

GenCore version 5.1.8  
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4 protein - protein search, using SW model

on on: May 15, 2006, 16:53:57 ; search time 145.923 seconds  
(without alignments)

376.380 Million cell updates/sec

title: US-10-041-860-48

perfect score: 672

sequence: 1 QVQLVQSGAEVKPAGASVTKVY.....YDYYGMDVWGQFTTVYSS 125

scoring table: BLOSUM62

Gappen 10.0 , Gapext 0.5

searched: 2443163 seqs, 439378781 residues

total number of hits satisfying chosen parameters: 2443163

ATTACHMENT S

**RESULT 1**  
**ADK18776** ADK18776 standard; protein; 125 AA.  
 XX  
**AC** ADK18776;  
 XX  
**DT** 06-MAY-2004 (first entry)  
 XX  
**DB** Anti-human PDGF-D antibody protein related sequence #2.  
 XX  
**KW** antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 XX  
**OS** Homo sapiens.  
 XX  
**PN** WO2003057857-A2.  
 XX  
**PD** 17-JUL-2003.  
 XX  
**PP** 06-JAN-2003; 2003WO-US000398.  
 XX  
**PR** 07-JAN-2002; 2002US-00041860.  
 XX  
**PA** (ABCE-) ABGENIX INC.  
 XX  
**PI** Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
**PI** Bezabeh B;  
 XX  
**DR** WPI; 2003-587119/55.  
 XX  
**PT** New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.  
 XX  
**PS** Disclosure; SEQ ID NO 200; 255pp; English.  
 XX  
**CC** The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the cDNA 3066418.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.  
 XX  
**SO** sequence 125 AA.

Prd. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SMARTES

Result No.	Score	Query Match	Length	DB ID	Description
1	672	100.0	125	7	ADKL8776 Anti-human
2	672	100.0	125	7	ADKL8948 Anti-human
3	672	100.0	125	7	ADKL8624 Anti-human
4	672	100.0	125	7	ADKL8813 Anti-human
5	672	100.0	125	8	ADL25392 Human mAb
6	638	94.9	125	7	ADKL8614 Anti-human
7	638	94.9	125	7	ADKL8779 Anti-human
8	638	94.9	125	7	ADKL8919 Anti-human
9	638	94.9	125	7	ADKL8816 Anti-human
10	638	94.9	125	8	ADL25444 Human mAb
11	593.5	88.3	126	7	ADKL8864 Anti-human
12	593.5	88.3	126	7	ADKL8595 Anti-human
13	593.5	88.3	126	7	ADKL8777 Anti-human
14	593.5	88.3	126	8	ADL25408 Human mAb
15	579.5	96.2	125	7	ADKL8814 Anti-human
16	575.5	85.6	126	7	ADKL8925 Anti-human
17	575.5	85.6	126	7	ADKL8780 Anti-human
18	575.5	85.6	126	7	ADKL8816 Anti-human
19	575.5	85.6	126	7	ADKL8817 Anti-human
20	575.5	85.6	126	8	ADL25448 Human mAb
21	572	95.1	127	7	ADKL8620 Anti-human
22	572	85.1	127	7	ADKL8818 Anti-human
23	572	85.1	127	7	ADKL8781 Anti-human
					Ad-18932 Anti-human





DT 06-MAY-2004 (first entry)  
 XX Anti-human PDGF-D antibody heavy chain protein sequence.  
 XX antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 XX Homo sapiens.  
 XX WO2003057857-A2.  
 XX PD 17-JUL-2003.  
 XX PR 06-JAN-2003; 2003WO-US000398.  
 XX PR 07-JAN-2002; 2002US-00041860.  
 XX PA (ABGENIX INC.  
 XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 XX PI Bezabeh B;  
 XX WPI; 2003-587119/55.  
 XX PR 07-JAN-2003; 2003WO-US000398.  
 XX PA (ABGENIX INC.  
 XX PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 XX PT Disclosure; SEQ ID NO 203; 255pp; English.  
 XX DR 2003-587119/55.  
 XX PT New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.  
 XX PT Disclosure; SEQ ID NO 38; 255pp; English.  
 XX CC The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.  
 XX PS Sequence corresponds to a protein used in the invention.  
 XX DR 2003-587119/55.  
 XX PT New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.  
 XX PT Disclosure; SEQ ID NO 38; 255pp; English.  
 XX CC The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCSP4/Sec-30664188. This sequence corresponds to a protein used in the invention.  
 XX SQ Sequence 125 AA:  
 Query Match 94.9%; Score 638; DB 7; Length 125;  
 Best Local Similarity 94.4%; Pred. No. 4.2e-51;  
 Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 QVQVJOSGAEVKKPKPASVVKVSCKASGYTFTSYDINWROATGQGLEMMGWNPNSGNTDY 60  
 Db 1 QVQLVOSGAEVKKPKPASVVKVSCKASGYTFTSYDINWROATGQGLEMMGWNPNSGNTGY 60  
 Qy 61 AQKPGQGRVMTTRDTTSITAYMELSSRSRDTAIVYCVRGFGSYNNYYGMDVWNGQRT 120  
 Db 61 AQKPGQGRVMTTRDTTSITAYMELSSRSRDTAIVYCVRGFGSYNNYYGMDVWNGQRT 120  
 Qy 61 AQKPGQGRVMTTRDTTSITAYMELSSRSRDTAIVYCVRGFGSYNNYYGMDVWNGQRT 120  
 Db 61 AQKPGQGRVMTTRDTTSITAYMELSSRSRDTAIVYCVRGFGSYNNYYGMDVWNGQRT 120  
 Qy 121 VTVSS 125  
 Db 121 VTVSS 125  
 XX RESULT 8  
 XX ADK18919 standard; protein; 125 AA.  
 XX AC ADK18919;  
 XX DT 06-MAY-2004 (first entry)  
 XX DB Anti-human PDGF-D antibody protein related sequence #145.  
 XX ID ADK18779;  
 XX DT 06-MAY-2004 (first entry)  
 XX DB Anti-human PDGF-D antibody protein related sequence #5.  
 XX KW antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 XX OS Homo sapiens.  
 XX PN WO2003057857-A2.  
 XX PD 17-JUL-2003.  
 XX PR 06-JAN-2003; 2003WO-US000398.  
 XX PR 07-JAN-2002; 2002US-00041860.  
 XX OS Homo sapiens.

(ABGE-) ABGENIX INC.  
 PA Corvalan JRF; Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;  
 XX WPI; 2003-587119/55.  
 New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. Disclosure: SEQ ID NO 343; 255pp; English.

CC The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid PCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

CC Sequence 125 AA;

Query Match 94.9%; Score 638; DB 7; Length 125;  
 Best Local Similarity 94.4%; Pred. No. 4.2e-51;  
 Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 SQ Sequence 125 AA;

Qy 1 QYLVQSGAETVKPGASVKSCASGTTSYDINWRAOTQGLEMGWNPNSGNTY 60  
 Db 1 QYLVQSGAETVKPGASVKSCASGTTSYDINWRAOTQGLEMGWNPNSGNTY 60

Qy 61 AQQFQGRVMTRDTSISTAYMELSSLEDTAIYCYRGFYSYNTDYYGMDVNGQTT 120  
 Db 61 AQQFQGRVMTRDTSISTAYMELSSLEDTAIYCYRGFYSYNTDYYGMDVNGQTT 120

Qy 121 VTVSS 125  
 Db 121 VTVSS 125

RESULT 9  
 ADK18816  
 ID ADK18816 standard; protein; 125 AA.  
 AC ADK18816;  
 DT 06-MAY-2004 (first entry)  
 DE Anti-human PDGF-D antibody protein related sequence #42.  
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 OS Homo sapiens.  
 PN WO2003057857-A2.

XX PR 17-JUL-2003.  
 XX PF 06-JAN-2003; 2003WO-US000398.

XX PR 07-JAN-2002; 2002US-00041860.  
 (ABGE-) ABGENIX INC.  
 PA Corvalan JRF; Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;

XX DR WPI; 2003-587119/55.  
 XX PT New human monoclonal antibody that binds to platelet-derived growth

PT factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.  
 PT Disclosure: SEQ ID NO 240; 255pp; English.  
 XX  
 CC The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid PCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

XX Sequence 125 AA;

Query Match 94.9%; Score 638; DB 7; Length 125;  
 Best Local Similarity 94.4%; Pred. No. 4.2e-51;  
 Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QYLVQSGAETVKPGASVKSCASGTTSYDINWRAOTQGLEMGWNPNSGNTY 60  
 Db 1 QYLVQSGAETVKPGASVKSCASGTTSYDINWRAOTQGLEMGWNPNSGNTY 60

Qy 61 AQQFQGRVMTRDTSISTAYMELSSLEDTAIYCYRGFYSYNTDYYGMDVNGQTT 120  
 Db 61 AQQFQGRVMTRDTSISTAYMELSSLEDTAIYCYRGFYSYNTDYYGMDVNGQTT 120

RESULT 10  
 ADL2544  
 ID ADL2544 standard; protein; 125 AA.  
 XX  
 AC ADL2544;  
 DT 17-JUN-2004 (first entry)  
 XX Human mAb 1.45 heavy chain variable region protein SEQ ID NO:54.  
 DE Human mAb 1.45 heavy chain variable region protein SEQ ID NO:54.  
 XX  
 KW antibody; binding fragment; platelet derived growth factor-**DD**; PDGF-**DD**; nephritis; mesangial cell proliferation inhibition; mesangial proliferative glomerulonephritis; nephrotropic; antiinflammatory; dermatological; immunosuppressive; antidiabetic; gene therapy; human; monoclonal antibody; mAb.  
 XX  
 OS Homo sapiens.  
 PN WO2004024098-A2.  
 XX  
 PD 25-MAR-2004.  
 XX  
 PF 16-SEP-2003; 2003WO-US009414.  
 XX  
 PR 16-SEP-2002; 2002US-0411137P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 PA (CURA-) CURAGEN CORP.  
 PA  
 PI Floege J, Gazit-Bornstein G, Keyt B, Larocheille WJ, Lichenstein H;  
 XX  
 DR WPI; 2004-269881/25.  
 DR N-PSDB; ADL25443.  
 XX  
 PT Use of an antibody or its binding fragment that binds platelet derived growth factor-**DD** (PDGF-**DD**) for preparing a medicament for treating nephritis.  
 PT  
 PT

PS Disclosure; SEQ ID NO 54; 115pp; English.

XX The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-**DD** (PDGF-**DD**), where the antibody is useful in preparing a medicament for treating nephritis. Also described: (1) a method of detecting nephritis; (2) a method of treating nephritis; (3) a method of inhibiting mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antifibrotic, dermatological, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-**DD**, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mAb) variable region sequence, which is used in the exemplification of the present invention.

XX Sequence 125 AA;

Query Match 94.9%; Score 638; DB 8; Length 125;  
Best Local Similarity 94.4%; Pred. No. 4.2e-51;  
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEYRKPGASVKVSKASGYTFSYDINWVQATGQGLEWMGNTDY 60  
Db 1 QVQLVQSGAEYRKPGASVKVSKASGYTFSYDINWVQATGQGLEWMGNTDY 60

Qy 61 AQKFGQRTMTRDTTSISTAYMELSSRSETDAAVYKTCRGYSSYDYYGMDWQGTT 120  
Db 61 AQKFGQRTMTRDTTSISTAYMELSSRSETDAAVYKTCRGYSSYDYYGMDWQGTT 120

Qy 121 TVVSS 125  
Db 121 TVVSS 125

RESULT 12  
ID ADK18595 standard; protein; 126 AA.  
XX ADK18595;  
AC ADK18595;  
XX 06-MAY-2004 (first entry)

XX Anti-human PDGF-D antibody heavy chain protein sequence.

XX DB Anti-human PDGF-D antibody; immunomodulator; cytostatic; gene therapy.

XX KW antiinflammatory; immunomodulator; cytostatic; gene therapy.

XX OS Homo sapiens.

XX PN WO2003057857-A2.

XX PD 17-JUL-2003.

XX PP 06-JAN-2003; 2003WO-US000398.

XX PR 07-JAN-2002; 2002US-00041860.

XX (ABGE-) ABGENIX INC.  
PA Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
PI Bezabeh B;  
XX DR 17-JUL-2003.  
XX PR 06-JAN-2003; 2003WO-US000398.  
XX PR 07-JAN-2002; 2002US-00041860.  
XX (ABGE-) ABGENIX INC.  
PA Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
PI Bezabeh B;  
XX DR 2003-587119/55.

XX New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.

XX PR New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.

XX PS Disclosure; SEQ ID NO 19; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCBP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

SQ	Sequence 126 AA;	Db	1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGMNPNSGNTGY 60
Query Match	88.3%; Score 593.5; DB 7; Length 126;	Qy	61 AQKFGQRVTMTRDTISIATAYMELSSLRSEDTAIVYCVR-GFGYSNYDYYGMDWQGQT 119
Best Local Similarity 89.7%; Pred. No. 5.4e-47; Mismatches 4; Indels 1; Gaps 1;		Db	61 AQKFGQRVTMTRDTISIATAYMELSSLRSEDTAIVYCVR-GFGYSNYDYYGMDWQGQT 119
Matches 113; Conservative		Qy	120 TTVVSS 125
Db	1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGMNPNSGNTGY 60	Db	121 TTVVSS 126
Qy	61 AQKFGQRVTMTRDTISIATAYMELSSLRSEDTAIVYCVR-GFGYSNYDYYGMDWQGQT 119	RESULT 14	
Db	61 AQKFGQRVTMTRDTISIATAYMELSSLRSEDTAIVYCVR-GFGYSNYDYYGMDWQGQT 120	ID	ADL25408 standard; protein; 126 AA.
Qy	120 TTVVSS 125	XX	XX
Db	121 TTVVSS 126	DT	17-JUN-2004 (first entry)
RESULT 13		XX	Human mAb 1.18 heavy chain variable region protein SEQ ID NO:18.
ADK18777		XX	DB
ID ADK18777 standard; protein; 126 AA.		XX	XX
XX		KW	antibody; binding fragment; platelet derived growth factor- <b>DD</b> ; PDGF- <b>DD</b> ;
AC ADK18777;		XX	nephritis; mesangial cell proliferation inhibition;
DT 06-MAY-2004 (first entry)		XX	mesangial proliferative glomerulonephritis; nephrotropic;
XX		KW	antiinflammatory; dermatological; immunosuppressive; antidiabetic;
DE Anti-human PDGF-D antibody protein related sequence #3.		XX	gene therapy; human; monoclonal antibody; mAb.
XX		OS	XX
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.		XX	Homosapiens.
XX		PN	XX
OS Homo sapiens.		PN02004024098-A2.	PN
XX		XX	W02004024098-A2.
OS Homo sapiens.		PD	XX
XX		25-MAR-2004.	PD
PN WO2003057857-A2.		XX	XX
XX		PP	16-SEP-2003; 2003WO-US039414.
PD 17-JUL-2003.		XX	XX
XX		PR	16-SEP-2002; 2002US-0411137P.
PP 06-JAN-2003; 2003WO-US000398.		XX	XX
XX		PA	(ABGE-) AGENIX INC.
PR 07-JAN-2002; 2002US-00041860.		XX	(CURA-) CURAGEN CORP.
XX		PI	XX
PA (ABGE-) AGENIX INC.		PI	Floeger J, Gazit-Bornstein G, Keyt B, Larchelle WJ, Lichenstein H;
PI Corvalan JRF, Jia X, Peng X, Yang X, Chen F, Gazit G, Weber R;		XX	XX
PI Bezabeh B;		DR	WPI; 2004-269081/25.
XX		DR	N-PSDB; ADL25407.
WPI; 2003-587119/55.		XX	XX
XX		PT	Use of an antibody or its binding fragment that binds platelet derived growth factor- <b>DD</b> (PDGF- <b>DD</b> ) for preparing a medicament for treating nephritis.
PT monocolonal antibody that binds to platelet-derived growth		PT	XX
PT factor- <b>DD</b> , useful for treating chronic and recurrent human		PT	Disclosure; SEQ ID NO 18; 115pp; English.
PT diseases, such as, inflammation, autoimmunity and cancer.		XX	XX
PS Disclosure; SEQ ID NO 201; 255pp; English.		CC	The present invention describes an antibody or its binding fragment that binds platelet derived growth factor- <b>DD</b> (PDGF- <b>DD</b> ), where the antibody is useful in preparing a medicament for treating nephritis. Also described:
XX		CC	(1) a method of detecting mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, immunosuppressive and antidiabetic activities and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF- <b>DD</b> , can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mAb) variable region sequence, which is used in the exemplification of the present invention.
PS		CC	XX
XX		CC	Sequence 126 AA;
PT		CC	Query Match 88.3%; Score 593.5; DB 8; Length 126;
PT		CC	Best Local Similarity 89.7%; Pred. No. 5.4e-47;
PT		CC	Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
PS Sequence 126 AA;		CC	Query 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGMNPNSGNTY 60
XX		CC	Query Match 88.3%; Score 593.5; DB 8; Length 126;
XX		CC	Best Local Similarity 89.7%; Pred. No. 5.4e-47;
XX		CC	Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Db	1	QVQLVQSGAEVYKPGASVKVSKASGYTFTSYDINWVQATGQGLEWMGMNPNSGNTGY	60	Db	123	VSS 125
Qy	61	AQKFQSRVITRDTISIATAYMELSSRLSERDTAVYTCVR-GFGYSNNDIYGMDWGQGT	119			
Db	61	AQKFQSRVITRDTISIATAYMELSSRLSERDTAVYTCVR-GFGYSNNDIYGMDWGQGT	119	Search completed: May 15, 2006, 16:58:54		
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Db	121	TVTVSS 126				
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		ADK18814				
		ID ADK18814 standard; protein; 125 AA.				
		XX				
		AC ADK18814;				
		XX				
		DT 06-MAY-2004 (first entry)				
		XX				
		Anti-human PDGF-D antibody protein related sequence #40.				
		XX				
		KW antiinflammatory; immunomodulator; cytostatic; gene therapy.				
		XX				
		OS Homo sapiens.				
		XX				
		PN WO2003057857-A2.				
		XX				
		PD 17-JUL-2003.				
		XX				
		PP 06-JAN-2003; 2003WO-US000398.				
		XX				
		PR 07-JAN-2002; 2002US-00041860.				
		XX				
		PA (ABGENIX INC.				
		XX				
		PI Corvalan JRF, Jia X, Peng X, Yang X, Chen F, Gazit G, Weber R;				
		XX				
		PI Bezabeh B;				
		XX				
		DR 2003-587119/55.				
		XX				
		New human monoclonal antibody that binds to platelet-derived growth				
		PT factor-D (PDGF-D), useful for treating chronic and recurrent human				
		PT diseases, such as, inflammation, autoimmunity and cancer.				
		XX				
		PS Disclosure: SEQ ID NO 238; 255pp; English.				
		XX				
		The invention relates to a human monoclonal antibody that binds to				
		CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for				
		CC treating chronic and recurrent human diseases, such as inflammation,				
		CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are				
		CC useful for modulating collagen formation, and for staging various				
		CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were				
		CC generated using an active protein fragment of the gene product from the				
		CC clone 3066188_0_99 arising in the conditioned medium obtained when				
		CC HEK293 cells are transfected with the plasmid PCBP4/Sec-30664188. This				
		CC sequence corresponds to a protein used in the invention.				
		XX				
		SQ Sequence 125 AA:				
		Query Match 86.2%; Score 579.5; DB 7; Length 125;				
		Best Local Similarity 89.4%; Pred. No. 1.1e-45;				
		Matches 110; Conservative 4; Mismatches 8; Indels 1; Gaps 1;				
Qy	4	LVQSGAVKKEPGASVKVSKASGYTFTSYDINWVQATGQGLEWMGMNPNSGNTGY	63			
Db	3	LVQSGAVKKEPGASVKVSKASGYTFTSYDINWVQATGQGLEWMGMNPNSGNTGY	62			
Qy	64	FQGRVITRDTISIATAYMELSSRLSERDTAVYTCVR-GFGYSNNDIYGMDWGQGT	122			
Db	63	FQGRVITRDTISIATAYMELSSRLSERDTAVYTCVR-GFGYSNNDIYGMDWGQGT	122			
Qy	123	VSS 125				

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 15, 2006, 17:04:12 ; Search time 35.4077 Seconds  
(without alignments)

291.870 Million cell updates/sec

Title: US-10-041-860-48

Perfect score: 672

Sequence: 1 QVQLVQSGAEVKKGASVRY.....YDYYGMDVWGQGTTVTVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 822675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541.5	80.6	120	2 US-09-025-769B-36	Sequence 36, App1
2	541.5	80.6	120	2 US-09-025-769B-59	Sequence 59, App1
3	541.5	80.6	120	2 US-09-490-070A-36	Sequence 36, App1
4	541.5	80.6	120	2 US-09-490-070A-59	Sequence 59, App1
5	541.5	80.6	120	2 US-09-490-153-36	Sequence 36, App1
6	541.5	80.6	120	2 US-09-490-153-59	Sequence 59, App1
7	541.5	80.6	120	2 US-09-490-324-36	Sequence 36, App1
8	541.5	80.6	120	2 US-09-490-324-59	Sequence 59, App1
9	528	78.6	117	2 US-09-025-769B-22	Sequence 22, App1
10	528	78.6	117	2 US-09-490-070A-22	Sequence 22, App1
11	528	78.6	117	2 US-09-490-153-22	Sequence 22, App1
12	528	78.6	117	2 US-09-490-324-22	Sequence 22, App1
13	526	78.3	470	2 US-09-859-053-28	Sequence 28, App1
14	513	76.3	125	2 US-09-490-149-3	Sequence 3, App1
15	510.5	76.0	128	1 US-08-204-047-22	Sequence 22, App1
16	510.5	76.0	128	2 US-08-964-690-22	Sequence 22, App1
17	510	75.9	129	1 US-08-561-521-45	Sequence 45, App1
18	510	75.9	129	2 US-08-535-539A-77	Sequence 77, App1
19	510	75.9	129	4 PCT-US95-01219-45	Sequence 45, App1
20	504	75.0	123	2 US-10-330-613A-21	Sequence 21, App1
21	502	74.7	123	1 US-08-477-877B-94	Sequence 94, App1
22	502	74.7	123	1 US-08-412-281A-94	Sequence 94, App1
23	502	74.7	123	1 US-08-477-983B-94	Sequence 94, App1
24	502	74.7	123	2 US-09-452-140D-102	Sequence 102, App1
25	502	74.7	123	2 US-09-452-140D-105	Sequence 105, App1
26	501	74.6	119	1 US-08-561-521-10	Sequence 10, App1
27	501	74.6	119	4 PCT-US95-01219-10	Sequence 10, App1

## ALIGNMENTS

RESULT 1  
US-09-025-769B-16

; Sequence 36, Application US/09025769B  
; Patent No. 6300064

; GENERAL INFORMATION:

; / APPLICANT: Knappik, Achim  
; / APPLICANT: Pack, Peter  
; / APPLICANT: Iлаг, Vic  
; / APPLICANT: Ge, Liming  
; / APPLICANT: Moroney, Simon  
; / APPLICANT: Pueckthun, Andreas  
; / TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; / NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; / ADDRESS: James P. Haley, Jr., Esq. c/o Fish & Neave  
; / STREET: 1251 Avenue of the Americas  
; / CITY: New York  
; / STATE: New York  
; / COUNTRY: USA  
; / ZIP: 10021

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIORITY APPLICATION DATA:  
; / APPLICATION NUMBER: EP 95 11 3021.0  
; / FILING DATE: 18-AUG-1995  
; / ATTORNEY/AGENT INFORMATION:  
; / NAME: James P. Haley, Jr., Esq.  
; / REGISTRATION NUMBER: 27,794  
; / REFERENCE/DOCKET NUMBER: MORPHO/5  
; / TELECOMMUNICATION INFORMATION:  
; / TELEPHONE: (212) 596-9000  
; / TELEFAX: (212) 596-9090  
; / INFORMATION FOR SEQ ID NO: 36:  
; / SEQUENCE CHARACTERISTICS:  
; / LENGTH: 120 amino acids  
; / TYPE: amino acid  
; / STRANDEDNESS:  
; / TOPOLOGY: linear  
; / MOLECULE TYPE: protein  
; / US-09-025-769B-16

Query Match 50.6%; Score 541.5; DB 2; Length 120;  
Best Local Similarity 84.0%; Pred. No. 1.7e-44;  
Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKKVSKASGYFTSYDINYVRAQTQGLEYWMGWINPNSGNTDY 60  
 Db 1 QVQLVQSGAEVKKPGASVKKVSKASGYFTSYDINYVRAQTQGLEYWMGWINPNSGNTY 60

RESULT 3  
 US-09-490-070A-36  
 Sequence 36, Application US/09490070A  
 ;  
 Patent No. 696248

GENERAL INFORMATION:  
 APPLICANT: Knappik, Achim  
 Pack, Peter  
 Ilag, Vic  
 Ge, Liming  
 Moroney, Simon  
 Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:  
 ADDRESSEES: Colin G. Sandercok, Esq. c/o Heller Ehrman  
 STREET: 1666 K Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20006

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/490,070A  
 FILING DATE: 24-Jan-2000  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:  
 NAME: Colin G. Sandercok, Esq.  
 REGISTRATION NUMBER: 31,798  
 REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 912-2000  
 TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 36:  
 LENGTH: 120 amino acids  
 TYPE: amino acid  
 STRANDBNESS: <Unknown>  
 TOPOLOGY: Linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
 US-09-490-070A-36

Query Match 80.6%; Score 541.5; DB 2; Length 120;  
 Best Local Similarity 84.0%; Pred. No. 1.7e-44;  
 Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKKVSKASGYFTSYDINYVRAQTQGLEYWMGWINPNSGNTY 60  
 Db 1 QVQLVQSGAEVKKPGASVKKVSKASGYFTSYDINYVRAQTQGLEYWMGWINPNSGNTY 60

RESULT 4  
 US-09-490-070A-59  
 Sequence 59, Application US/09490070A  
 ;

Qy 1 QVQLVQSGAEVKKPGASVKKVSKASGYFTSYDINYVRAQTQGLEYWMGWINPNSGNTY 60  
 Db 1 QVQLVQSGAEVKKPGASVKKVSKASGYFTSYDINYVRAQTQGLEYWMGWINPNSGNTY 60

Qy 61 AQKFGQRTMTRDTISIAYMELSSRSEDAIYCYCVRGFGSYNVDYCCMDVNGQGTT 120  
 Db 61 AQKFGQRTMTRDTISIAYMELSSRSEDAIYCYCVRGFGSYNVDYCCMDVNGQGTT 120

Qy 121 VTVSS 125  
 Db 116 VTVSS 120

Qy 121 VTVSS 125

Patent No. 6696248  
 GENERAL INFORMATION:  
 APPLICANT: Knappik, Achim  
 Pack, Peter  
 Ilag, Vic  
 Ge, Liming  
 Moroney, Simon  
 Plueckthun, Andreas  
 TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CORRESPONDENCE ADDRESS:  
 ADDRESSSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
 White & McAuliffe  
 STREET: 1666 K Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20006  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/490,070A  
 FILING DATE: 24-Jan-2000  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Colin G. Sandercock, Esq.  
 REGISTRATION NUMBER: 31,298  
 REFERENCE/DOCKET NUMBER: 37629-0005  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 912-2000  
 TELEFAX: (202) 912-2020  
 INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 120 amino acids  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
 US-09-490-070A-59

Query Match 80.6%; Score 541.5; DB 2; Length 120;  
 Best Local Similarity 84.0%; Pred. No. 1.7e-44;  
 Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

Qy 1 QYQLVQSGAEVTKPGASVKVSKASGTYFTSYDINNYRQATCQGLEMMGWNPNSGNTDY 60  
 Db 1 QYQLVQSGAEVTKPGASVKVSKASGTYFTSYDINNYRQATCQGLEMMGWNPNSGNTDY 60

Qy 1 QYQLVQSGAEVTKPGASVKVSKASGTYFTSYDINNYRQATCQGLEMMGWNPNSGNTDY 60  
 Db 1 QYQLVQSGAEVTKPGASVKVSKASGTYFTSYDINNYRQATCQGLEMMGWNPNSGNTDY 60

Qy 61 AOKPQGRVTTMTRDTTSIATMELSLRSRSEDATAVYCARWGG 120  
 Db 61 AOKPQGRVTTMTRDTTSIATMELSLRSRSEDATAVYCARWGG 115

RESULT 6  
 US-09-490-153-59  
 / Sequence 59, Application US/09490153  
 / Patent No. 6706484  
 / GENERAL INFORMATION:  
 / APPLICANT: Knappik, Achim  
 / Pack, Peter  
 / Ilag, Vic  
 / Ge, Liming  
 / Moroney, Simon  
 / Plueckthun, Andreas  
 / TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 / NUMBER OF SEQUENCES: 373  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 / STREET: 1251 Avenue of the Americas  
 / CITY: New York  
 / STATE: New York  
 / COUNTRY: USA  
 / ZIP: 10021

Query Match 80.6%; Score 541.5; DB 2; Length 120;  
 Best Local Similarity 84.0%; Pred. No. 1.7e-44;  
 Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

Qy 1 QYQLVQSGAEVTKPGASVKVSKASGTYFTSYDINNYRQATCQGLEMMGWNPNSGNTDY 60  
 Db 1 QYQLVQSGAEVTKPGASVKVSKASGTYFTSYDINNYRQATCQGLEMMGWNPNSGNTDY 60

Qy 61 AOKPQGRVTTMTRDTTSIATMELSLRSRSEDATAVYCARWGG 120  
 Db 61 AOKPQGRVTTMTRDTTSIATMELSLRSRSEDATAVYCARWGG 115

RESULT 6  
 US-09-490-153-59  
 / Sequence 59, Application US/09490153  
 / Patent No. 6706484  
 / GENERAL INFORMATION:  
 / APPLICANT: Knappik, Achim  
 / Pack, Peter  
 / Ilag, Vic  
 / Ge, Liming  
 / Moroney, Simon  
 / Plueckthun, Andreas  
 / TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 / NUMBER OF SEQUENCES: 373  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 / STREET: 1251 Avenue of the Americas  
 / CITY: New York  
 / STATE: New York  
 / COUNTRY: USA  
 / ZIP: 10021

RESULT 5  
 US-09-490-153-36  
 / Sequence 36, Application US/09490153  
 / Patent No. 6706484  
 / GENERAL INFORMATION:  
 / APPLICANT: Knappik, Achim  
 / Pack, Peter  
 / Ilag, Vic  
 / Ge, Liming  
 / Moroney, Simon  
 / Plueckthun, Andreas

STATE: New York  
 CITY: USA  
 ZIP: 10021  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/490,153  
 FILING DATE: 24-Jan-2000  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/09/025,769B  
 FILING DATE: 18-FEB-1998  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: James F. Haley, Jr., BBQ.  
 REGISTRATION NUMBER: 27 794  
 REFERENCE/DOCKET NUMBER: MORPHO/5  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 596-9000  
 TELEFAX: (212) 596-9090  
 INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 120 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
 US-09-490-153-59

Query Match 80.6%; Score 541.5; DB 2; Length 120;  
 Best Local Similarity 84.0%; Pred. No. 1.7e-44;  
 Matches 105; Conservative 5; Mismatches 10; Indels 5

Qy 1 QVQLVSGAELYRKPGASVVKSCASGTYFTSYDINWROATGQHLEWMGIVIN  
 Db 1 QVQLVSGAELYRKPGASVVKSCASGTYFTSYDINWROATGQHLEWMGIVIN

Qy 61 AQKFGQRVTMTRDTSTSTAYMELSSRSRSETAAYCVRGFGYSNYDYYGMMI  
 Db 61 AQKFGQRVTMTRDTSTSTAYMELSSRSRSETAAYCVRGFGYSNYDYYGMMI

Qy 121 VTVSS 125  
 Db 116 VTVSS 120

RESULT 7  
 US-09-490-324-36  
 Sequence 36. Application US/09490324  
 Patent No. 6828422  
 GENERAL INFORMATION:  
 APPLICANT: Knappik, Achim  
 Pack, Peter  
 Ilag, Vic  
 Ge, Liming  
 Moroney, Simon  
 Plueckthun, Andreas  
 TITLE OF INVENTION: Protein/ (Poly) peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10021  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA: US/09/490,324

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acid(s)

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 36:

US-09-490-324-36

	Query	Macch	Score	DB 2;	Length
	Best	Local	Similarity	Pred. No.	17e-44;
	Matches	105;	Conservative	Mismatches	Indels
Qy	1	QVQLVQSGAEVKPGASVKVSKAGSFTPSYDINWVROTQGGLIEWMGW	80.6%	541.5;	120;
Db	1	QVQLVQSGAEVKPGASVKVSKAGSFTPSYDINWVROTQGGLIEWMGW	84.0%;	Pred. No. 1.7e-10;	
Qy	61	AQKFGQRVTMTRDTISIATMELSSLRSEDATAIYCVRGPGSYNDDY	1	5;	
Db	61	AQKFGQRVTMTRDTISIATMELSSLRSEDATAIYCVRGPGSYNDDY	1	5;	
Qy	121	VTVSS 125	1	5;	
Db	116	VTVSS 120	1	5;	

RESULT 8

US-09-490-324-59

Sequence 59, Application US/09490324

Patent No. 682842

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neau

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769



SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-09-490-070A-22

Query Match 78.6%; Score 528; DB 2; Length 117;  
Best Local Similarity 82.5%; Pred. No. 3 2e-43;  
Matches 104; Conservative 5; Mismatches 7; Indels 10; Gaps 2;

Qy 1 QVQLVSGAELYKKPGASVKVSKASGYTFTSYDINWVROATGOGIIEWMGWNPNSGNTDY 60  
Db 1 QVQLVSGAELYKKPGASVKVSKASGYTFTSYDINWVROATGOGIIEWMGWNPNSGNTNY 60

Qy 1 QVQLVSGAELYKKPGASVKVSKASGYTFTSYDINWVROATGOGIIEWMGWNPNSGNTDY 60  
Db 1 QVQLVSGAELYKKPGASVKVSKASGYTFTSYDINWVROATGOGIIEWMGWNPNSGNTNY 60

Qy 61 AQKPGQRTVMTRDTSISTAYMELSLRSDDTAVYCARDG-----GFDWQGQT 119  
Db 1 AQKPGQRTVMTRDTSISTAYMELSLRSDDTAVYCARDG-----GFDWQGQT 119

Qy 120 TVTVSS 125  
Db 112 TVTVSS 117

RESULT 12  
US-09-490-324-22

Sequence 22, Application US/09490324  
Patent No. 6828422

GENERAL INFORMATION:

APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly) peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: MORPHO/5  
TELEPHONE: (212)596-9090

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-09-490-324-22

Query Match 78.6%; Score 528; DB 2; Length 117;  
Best Local Similarity 82.5%; Pred. No. 3 2e-43;  
Matches 104; Conservative 5; Mismatches 7; Indels 10; Gaps 2;

Qy 1 QVQLVSGAELYKKPGASVKVSKASGYTFTSYDINWVROATGOGIIEWMGWNPNSGNTDY 60  
Db 1 QVQLVSGAELYKKPGASVKVSKASGYTFTSYDINWVROATGOGIIEWMGWNPNSGNTNY 60

Qy 1 QVQLVSGAELYKKPGASVKVSKASGYTFTSYDINWVROATGOGIIEWMGWNPNSGNTDY 60  
Db 1 QVQLVSGAELYKKPGASVKVSKASGYTFTSYDINWVROATGOGIIEWMGWNPNSGNTNY 60

Qy 61 AQKPGQRTVMTRDTSISTAYMELSLRSDDTAVYCARDG-----GFDWQGQT 119  
Db 1 AQKPGQRTVMTRDTSISTAYMELSLRSDDTAVYCARDG-----GFDWQGQT 119

Db 61 AQRFGRTVMTRTSISIAYMELSSRLRSDDTAVYCARQDG-----GFDYNGQGT 111  
 Qy 120 VTVYSS 125  
 Db 112 Lvtvss 117

RESULT 1.3  
 US-09-859-053-28  
 ; Sequence 28, Application US/09859053  
 ; Patent No. 6803039  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tsuji, Takashi  
 ; APPLICANT: Teruha, Katsunari  
 ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
 ; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND  
 ; FILE REFERENCE: 06/301-079001  
 ; CURRENT APPLICATION NUMBER: US/09/859,053  
 ; CURRENT FILING DATE: 2001-05-16  
 ; PRIOR APPLICATION NUMBER: JP 2001-99508  
 ; PRIOR FILING DATE: 2001-03-30  
 ; PRIOR APPLICATION NUMBER: JP 2000-147116  
 ; PRIOR FILING DATE: 2000-05-18  
 ; NUMBER OF SEQ ID NOS: 43  
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0  
 ; SEQ ID NO: 28  
 ; LENGTH: 470  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-859-053-28

Query Match 78.3%; Score 526; DB 2; Length 470;  
 Best Local Similarity 79.2%; Prod. No. 2.e-4;  
 Matches 99; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPGASVKVSKASGTTFTSDINWVQATQGLEMWGWINPNSNTDY 60  
 Db 20 QVQLVQSGAEVKPGASVKVSKASGTTFTGTYMMWVQATQGLEMWGWINPNSGTT 79  
 Qy 61 AQRFGRTVMTRTSISIAYMELSSRLRSDDTAVYCARQDG-----GFDYNGQGT 120  
 Db 80 AQRFGRTVMTRTSISIAYMELSSRLRSDDTAVYCARQDG-----GFDYNGQGT 139  
 Qy 121 VTVYSS 125  
 Db 140 VTVYSS 144

RESULT 14  
 US-09-199-149-3  
 ; Sequence 3, Application US/09199149  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jonak, Zdenka L.  
 ; APPLICANT: Taylor, Alexander H.  
 ; APPLICANT: Trulli, Jr., Stephen H.  
 ; APPLICANT: Johansson, Kyung O.  
 ; TITLE OF INVENTION: Humanized Monoclonal Antibodies  
 ; FILE REFERENCE: P50860  
 ; CURRENT APPLICATION NUMBER: US/09/199,149  
 ; CURRENT FILING DATE: 1998-11-24  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 3  
 ; LENGTH: 125  
 ; TYPE: PRT  
 ; ORGANISM: Kabat VH subgroup I  
 US-09-199-149-3

Query Match 76.3%; Score 513; DB 2; Length 125;

Db 1 QVQLVQSGAEVKPGASVKVSKASGTTFTSDINWVQATQGLEMWGWINPNSGTT 59  
 1 QVQLVQSGAEVKPGASVKVSKASGTTFTSIAISWVQATQGLEMWGWINPNSGDTN 60

Best Local Similarity 80.6%; Prod. No. 9.3e-42;  
 Matches 104; Conservative 8; Mismatches 9; Indels 8; Gaps 5;

Qy 1 QVQLVQSGAEVKPGASVKVSKASGTTFTSDINWVQATQGLEMWGWINPNSNTDY 60  
 Db 1 QVQLVQSGAEVKPGASVKVSKASGTTFTSIAISWVQATQGLEMWGWINP-GGDTNY 59  
 Qy 61 AQRFGRTVMTRTSISIAYMELSSRLRSDDTAVYCARQDG-----GFDYNGQGT 116  
 Db 60 AQRFGRTVMTRTSISIAYMELSSRLRSDDTAVYCARPGTYGGCCYGY-WYWG--WVG 116  
 Qy 117 QGTVTVSS 125  
 Db 117 QGTVTVSS 125

RESULT 15  
 US-08-202-047-22  
 ; Sequence 22, Application US/08202047  
 ; Patent No. 5800815  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHERNUT, Robert W.  
 ; APPLICANT: POLLIE, Margaret J.  
 ; APPLICANT: PAULSON, James C.  
 ; APPLICANT: JONES, S. Tarran  
 ; APPLICANT: SALDANHA, Jose W.  
 ; APPLICANT: BENDIG, Mary M.  
 ; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew  
 ; STREET: One Market Plaza, Stewart Tower, Suite 2000  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/202,047  
 ; FILING DATE: 25-FEB-1994  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, William M.  
 ; REGISTRATION NUMBER: 30,223  
 ; REFERENCE/DOCKET NUMBER: 14137-77  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-326-24200  
 ; TELEFAX: 415-326-2422  
 ; INFORMATION FOR SEQ ID NO: 22:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 128 amino acids  
 ; TYPE: amino acid  
 ; STRANDBEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FEATURE:  
 ; NAME/KEY: Protein  
 ; LOCATION: 1-128  
 ; OTHER INFORMATION: /label= HUMAN\_I  
 US-08-202-047-22

Query Match 76.0%; Score 510.5; DB 1; Length 128;  
 Best Local Similarity 77.9%; Prod. No. 1.e-41;  
 Matches 102; Conservative 7; Mismatches 13; Indels 9; Gaps 3;

Qy 1 QVQLVQSGAEVKPGASVKVSKASGTTFTSDINWVQATQGLEMWGWINPNSGTT 59  
 1 QVQLVQSGAEVKPGASVKVSKASGTTFTSIAISWVQATQGLEMWGWINPNSGDTN 60

Qy 60 YAQKFOGRVMTRDTSISAYMELSSLRSEDTAYCVRGFGS---YNYDYYGMDV 114  
Db 61 YAQKFQERVITADTSISAYMELSSLRSEDTAVYCARAFYGSQGCTRGDFP---Dy 117

Qy 115 WGQGTTTVSS 125  
Db 118 WGQGTTTVSS 128

Search completed: May 15, 2006, 17:06:02  
Job time : 36.4077 sec<sub>8</sub>

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OM protein - protein search, using sw model

Run on: May 15, 2006, 17:19:47 ; Search time 126.073 Seconds (without alignment(s)) 414.273 Million cell updates/sec

Title: US-10-041-860-48

Perfect score: 672

Sequence: 1 QVQLVQSGAEVKKEKGASVYKV.....YDYYGMDVWGQGTIVTVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 % Maximum Match 100% Listing First 45 summaries

Database : Published Applications \_AA\_Main:\* 1: /cgn2\_6/\_ptodata/1/\_pubpaa/\_US07\_PUBCOMB.pep: \* 2: /cgn2\_6/\_ptodata/1/\_pubpaa/\_US08\_PUBCOMB.pep: \* 3: /cgn2\_6/\_ptodata/1/\_pubpaa/\_US09\_PUBCOMB.pep: \* 4: /cgn2\_6/\_ptodata/1/\_pubpaa/\_US10A\_PUBCOMB.pep: \* 5: /cgn2\_6/\_ptodata/1/\_pubpaa/\_US10B\_PUBCOMB.pep: \* 6: /cgn2\_6/\_ptodata/1/\_pubpaa/\_US11\_PUBCOMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	672	100.0	125	4	US-10-041-860-48
2	672	100.0	125	4	US-10-041-860-200
3	672	100.0	125	4	US-10-041-860-237
4	672	100.0	125	4	US-10-041-860-372
5	672	100.0	125	4	US-10-041-860-383-2
6	638	94.9	125	4	US-10-041-860-38
7	638	94.9	125	4	US-10-041-860-203
8	638	94.9	125	4	US-10-041-860-240
9	638	94.9	125	4	US-10-041-860-343
10	638	94.9	125	4	US-10-041-860-343
11	593.5	88.3	126	4	US-10-041-860-19
12	593.5	88.3	126	4	US-10-041-860-201
13	593.5	88.3	126	4	US-10-041-860-288
14	593.5	88.3	126	4	US-10-041-860-318
15	579.5	86.2	125	4	US-10-041-860-238
16	575.5	85.6	126	4	US-10-041-860-40
17	575.5	85.6	126	4	US-10-041-860-204
18	575.5	85.6	126	4	US-10-041-860-241
19	575.5	85.6	126	4	US-10-041-860-349
20	575.5	85.6	126	4	US-10-041-860-58
21	572	85.1	127	4	US-10-041-860-44
22	572	85.1	127	4	US-10-041-860-205
23	572	85.1	127	4	US-10-041-860-242
24	572	85.1	127	4	US-10-041-860-360
25	572	85.1	127	4	US-10-041-860-333-66
26	567.5	84.4	126	4	US-10-041-860-21
27	567.5	84.4	126	4	US-10-041-860-199

RESULT 1  
US-10-041-860-48  
; Sequence 48, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; INVENTOR: Corvalan, Jose R.F.  
; ADDRESS: 162, APP  
; SEQUENCE: 162, APP  
; SEQUENCE: 101, APP  
; SEQUENCE: 124, APP  
; SEQUENCE: 103, APP  
; SEQUENCE: 79, APP  
; SEQUENCE: 46, APP  
; SEQUENCE: 3, APP  
; SEQUENCE: 3, APP  
; ALIGNMENTS

Query Match 100.0% ; Score 672; DB 4; Length 125;  
Best Local Similarity 100.0%; Pred. No. 8.6e-54;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-041-860-48  
Query Match 100.0% ; Score 672; DB 4; Length 125;  
Best Local Similarity 100.0%; Pred. No. 8.6e-54;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-041-860-48  
Qy 1 QVQLVQSGAEVKKEKGASVYKTVSS 125  
Db 1 QVQLVQSGAEVKKEKGASVYKTVSS 125  
Qy 1 QVQLVQSGAEVKKEKGASVYKTVSS 125  
Db 1 QVQLVQSGAEVKKEKGASVYKTVSS 125  
Qy 61 AQKFQGRVITRDTISIATMELSSRSEDTAIYVCKGASVYKKEKGASVYKTVSS 120  
Db 61 AQKFQGRVITRDTISIATMELSSRSEDTAIYVCKGASVYKKEKGASVYKTVSS 120  
Qy 121 VTVSS 125  
Db 121 VTVSS 125  
RESULT 2  
US-10-041-860-200  
; Sequence 200, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; INVENTOR: Corvalan, Jose R.F.  
; ADDRESS: 162, APP

1 APPLICANT: Feng, Xiao  
 1 APPLICANT: Yang, Xiao-Dong  
 1 APPLICANT: Chen, Francine  
 1 APPLICANT: Gazit, Gadi  
 1 APPLICANT: Weber, Richard  
 1 TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
 1 TITLE OF INVENTION: THEREOF  
 1 FILE REFERENCE: AGENIX.051A  
 1 CURRENT APPLICATION NUMBER: US/10/041,860  
 1 CURRENT FILING DATE: 2002-01-07  
 1 SOFTWARE: FastSEQ for Windows Version 4.0  
 1 SEQ ID NO: 200  
 1 LENGTH: 125  
 1 TYPE: PRT  
 1 ORGANISM: homo sapiens  
 1 US-10-041-860-200

Query Match 100.0%; Score 672; DB 4; Length 125;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-54;  
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQGAEVKPGASVKVSKASGFTSYDINVRQATQGLEWMGWMNPNSGNTDY 60  
 Db 1 QVQLVQGAEVKPGASVKVSKASGFTSYDINVRQATQGLEWMGWMNPNSGNTDY 60

Qy 61 AQQFQGRVTMIRDTSISTAYMELSSLRSEDAIYCYCVRGFGSYNTYYGMDVWQGTT 120  
 Db 61 AQQFQGRVTMIRDTSISTAYMELSSLRSEDAIYCYCVRGFGSYNTYYGMDVWQGTT 120

Qy 121 VTVSS 125  
 Db 121 VTVSS 125

RESULT 3  
 US-10-041-860-237  
 1 Sequence 37, Application US/10041860  
 1 Publication No. US20030157109A1  
 1 GENERAL INFORMATION:  
 1 APPLICANT: Corvalan, Jose R. P.  
 1 APPLICANT: Jia, Xiao-Chi  
 1 APPLICANT: Feng, Xiao  
 1 APPLICANT: Yang, Xiao-Dong  
 1 APPLICANT: Chen, Francine  
 1 APPLICANT: Gazit, Gadi  
 1 APPLICANT: Weber, Richard  
 1 TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
 1 TITLE OF INVENTION: THEREOF  
 1 FILE REFERENCE: AGENIX.051A  
 1 CURRENT APPLICATION NUMBER: US/10/041,860  
 1 CURRENT FILING DATE: 2002-01-07  
 1 NUMBER OF SEQ ID NOS: 377  
 1 SOFTWARE: FastSEQ for Windows Version 4.0  
 1 SEQ ID NO: 237  
 1 LENGTH: 125  
 1 TYPE: PRT  
 1 ORGANISM: homo sapiens  
 1 US-10-041-860-237

Query Match 100.0%; Score 672; DB 4; Length 125;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-54;  
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQGAEVKPGASVKVSKASGFTSYDINVRQATQGLEWMGWMNPNSGNTDY 60  
 Db 1 QVQLVQGAEVKPGASVKVSKASGFTSYDINVRQATQGLEWMGWMNPNSGNTDY 60

Qy 61 AQQFQGRVTMIRDTSISTAYMELSSLRSEDAIYCYCVRGFGSYNTYYGMDVWQGTT 120  
 Db 61 AQQFQGRVTMIRDTSISTAYMELSSLRSEDAIYCYCVRGFGSYNTYYGMDVWQGTT 120

Qy 121 VTVSS 125  
 Db 121 VTVSS 125

RESULT 4  
 US-10-041-860-372  
 1 Sequence 372, Application US/10041860  
 1 Publication No. US20030157109A1  
 1 GENERAL INFORMATION:  
 1 APPLICANT: Corvalan, Jose R. P.  
 1 APPLICANT: Jia, Xiao-Chi  
 1 APPLICANT: Feng, Xiao  
 1 APPLICANT: Yang, Xiao-Dong  
 1 APPLICANT: Chen, Francine  
 1 APPLICANT: Gazit, Gadi  
 1 APPLICANT: Weber, Richard  
 1 APPLICANT: Bezbah, Binyamin  
 1 TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
 1 TITLE OF INVENTION: THEREOF  
 1 FILE REFERENCE: AGENIX.051A  
 1 CURRENT APPLICATION NUMBER: US/10/041,860  
 1 CURRENT FILING DATE: 2002-01-07  
 1 NUMBER OF SEQ ID NOS: 377  
 1 SOFTWARE: FastSEQ for Windows Version 4.0  
 1 SEQ ID NO: 312  
 1 LENGTH: 125  
 1 TYPE: PRT  
 1 ORGANISM: homo sapiens  
 1 US-10-041-860-372

Query Match 100.0%; Score 672; DB 4; Length 125;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-54;  
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQGAEVKPGASVKVSKASGFTSYDINVRQATQGLEWMGWMNPNSGNTDY 60  
 Db 1 QVQLVQGAEVKPGASVKVSKASGFTSYDINVRQATQGLEWMGWMNPNSGNTDY 60

Qy 61 AQQFQGRVTMIRDTSISTAYMELSSLRSEDAIYCYCVRGFGSYNTYYGMDVWQGTT 120  
 Db 61 AQQFQGRVTMIRDTSISTAYMELSSLRSEDAIYCYCVRGFGSYNTYYGMDVWQGTT 120

Qy 121 VTVSS 125  
 Db 121 VTVSS 125

RESULT 5  
 US-10-665-383-2  
 1 Sequence 2, Application US/10665383  
 1 Publication No. US20040141969A1  
 1 GENERAL INFORMATION:  
 1 APPLICANT: Ploeg, Juergen  
 1 APPLICANT: Gazit, Gadi  
 1 APPLICANT: Keyt, Bruce  
 1 APPLICANT: LaRochelle, William  
 1 APPLICANT: Lichtenstein, Henri  
 1 TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS  
 1 TITLE OF INVENTION: USING ANTI-PDGFD ANTIBODIES  
 1 FILE REFERENCE: AGENIX.052A  
 1 CURRENT APPLICATION NUMBER: US/10/665,383  
 1 CURRENT FILING DATE: 2003-09-16  
 1 PRIOR APPLICATION NUMBER: 60/411,137  
 1 PRIOR FILING DATE: 2002-09-16  
 1 NUMBER OF SEQ ID NOS: 97  
 1 SOFTWARE: FastSEQ for Windows Version 4.0  
 1 SEQ ID NO: 2  
 1 LENGTH: 125  
 1 TYPE: PRT  
 1 ORGANISM: homo sapiens  
 1 US-10-665-383-2

Query Match 100.0%; Score 672; DB 4; Length 125;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-54;  
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQGAEVKPGASVKVSKASGFTSYDINVRQATQGLEWMGWMNPNSGNTDY 60  
 Db 1 QVQLVQGAEVKPGASVKVSKASGFTSYDINVRQATQGLEWMGWMNPNSGNTDY 60

Qy 61 AQQFQGRVTMIRDTSISTAYMELSSLRSEDAIYCYCVRGFGSYNTYYGMDVWQGTT 120  
 Db 61 AQQFQGRVTMIRDTSISTAYMELSSLRSEDAIYCYCVRGFGSYNTYYGMDVWQGTT 120



RESULT 9  
 US-10-041-860-343  
 ; Sequence 343, Application US/10041860  
 ; Publication No. US20030157109A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Corvalan, Jose R.F.  
 ; APPLICANT: Jia, Xiao-Chi  
 ; APPLICANT: Peng, Xiao  
 ; APPLICANT: Yang, Xiao-Dong  
 ; APPLICANT: Chen, Francine  
 ; APPLICANT: Gazi, Gadi  
 ; APPLICANT: Weber, Richard  
 ; APPLICANT: Bezabeh, Binyam  
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: AGENIX.051A  
 ; CURRENT APPLICATION NUMBER: US/10/041,860  
 ; CURRENT FILING DATE: 2002-01-07  
 ; NUMBER OF SEQ ID NOS: 377  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 343  
 ; LENGTH: 125  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 ; US-10-041-860-343

Query Match 94.9%; Score 638; DB 4; Length 125;  
 Best Local Similarity 94.4%; Pred. No. 1.1e-50;  
 Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKSCKASGYFTSYDINWROATGQLEWMGWINPNSGNTY 60  
 Db 1 QVQLVQSGAEVKKPGASVKSCKASGYFTSYDINWROATGQLEWMGWINPNSGNTY 60

Qy 61 AQKFGQRTMTRDTS1STAYMELSSLRSEDTAIXYCVRGFYSYNYDYYGMDWQGTT 120  
 Db 61 AQKFGQRTMTRDTS1STAYMELSSLRSEDTAIVYCARGSGSYCYDYYGMDWQGTT 120

Qy 121 VTVSS 125  
 Db 121 VTVSS 125

RESULT 10  
 US-10-665-383-54  
 ; Sequence 54, Application US/10665383  
 ; Publication No. US20040141969A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Floege, Juergen  
 ; APPLICANT: Gazi, Gadi  
 ; APPLICANT: Keyt, Bruce  
 ; APPLICANT: LaRochelle, William  
 ; APPLICANT: Lichtenstein, Henri  
 ; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS  
 ; FILE REFERENCE: AGENIX.052A  
 ; CURRENT APPLICATION NUMBER: US/10/665,383  
 ; CURRENT FILING DATE: 2003-09-16  
 ; PRIOR APPLICATION NUMBER: 60/411,137  
 ; PRIOR FILING DATE: 2003-09-16  
 ; NUMBER OF SEQ ID NOS: 97  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 54  
 ; LENGTH: 125  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 ; US-10-665-383-54

Query Match 94.9%; Score 638; DB 4; Length 125;  
 Best Local Similarity 94.4%; Pred. No. 1.1e-50;  
 Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

RESULT 11  
 US-10-041-860-19  
 ; Sequence 19, Application US/10041860  
 ; Publication No. US20030157109A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Corvalan, Jose R.F.  
 ; APPLICANT: Jia, Xiao-Chi  
 ; APPLICANT: Feng, Xiao  
 ; APPLICANT: Yang, Xiao-Dong  
 ; APPLICANT: Chen, Francine  
 ; APPLICANT: Gazi, Gadi  
 ; APPLICANT: Weber, Richard  
 ; APPLICANT: Bezabeh, Binyam  
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: AGENIX.051A  
 ; CURRENT APPLICATION NUMBER: US/10/041,860  
 ; CURRENT FILING DATE: 2002-01-07  
 ; NUMBER OF SEQ ID NOS: 377  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 19  
 ; LENGTH: 126  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 ; US-10-041-860-19

Query Match 88.3%; Score 593.5; DB 4; Length 126;  
 Best Local Similarity 89.7%; Pred. No. 1.3e-46;  
 Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKSCKASGYFTSYDINWROATGQLEWMGWINPNSGNTY 60  
 Db 1 QVQLVQSGAEVKKPGASVKSCKASGYFTSYDINWROATGQLEWMGWINPNSGNTY 60

Qy 61 AQKFGQRTMTRDTS1STAYMELSSLRSEDTAIXYCVRGFYSYNYDYYGMDWQGTT 119  
 Db 61 AQKFGQRTMTRDTS1STAYMELSSLRSEDTAIVYCARGSGSYCYDYYGMDWQGTT 120

Qy 120 VTVSS 125  
 Db 121 VTVSS 126

RESULT 12  
 US-10-041-860-201  
 ; Sequence 201, Application US/10041860  
 ; Publication No. US20030157109A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Corvalan, Jose R.F.  
 ; APPLICANT: Jia, Xiao-Chi  
 ; APPLICANT: Feng, Xiao  
 ; APPLICANT: Yang, Xiao-Dong  
 ; APPLICANT: Chen, Francine  
 ; APPLICANT: Gazi, Gadi  
 ; APPLICANT: Weber, Richard  
 ; APPLICANT: Bezabeh, Binyam  
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: AGENIX.051A  
 ; CURRENT APPLICATION NUMBER: US/10/041,860

CURRENT FILING DATE: 2002-01-07  
 NUMBER OF SEQ ID NOS: 377  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 201  
 LENGTH: 126  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-10-041-860-201

Query Match 88.3%; Score 593.5; DB 4; Length 126;  
 Best Local Similarity 89.7%; Pred. No. 1.3e-46;  
 Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;  
 Matches 113; Conservation 4; Mismatches 8; Indels 1; Gaps 1;

Qy 1 QVQLVQSAEVKKPGASVKSCKASGTTFTSDINWVQATQGGLEMMGWINPNSGNTDY 60  
 Db 1 QVQLVQSAEVKKPGASVKSCKASGTTFTSDINWVQATQGGLEMMGWINPNSGNTGY 60  
 Qy 61 AOKPQGRVTMTRDTISIATAYMELLSLRSEDTAIYCYVR-GFGYSYNYDYYGMDVNGQT 119  
 Db 61 AOKPQGRVTMTRNTISIATAYMELLSLRSEDTAIYCYVR-GFGYSYNYDYYGMDVNGQT 120

Qy 120 TVTVSS 125  
 Db 121 TVTVSS 126

RESULT 13  
 US-10-041-860-288  
 Sequence 288, Application US/10041860  
 Publication No. US20030157109A1  
 GENERAL INFORMATION  
 APPLICANT: Corvalan, Jose R.P.  
 APPLICANT: Jia, Xiao-Chi  
 APPLICANT: Feng, Xiao  
 APPLICANT: Yang, Xiao-Dong  
 APPLICANT: Chen, Francine  
 APPLICANT: Gazit, Gadi  
 APPLICANT: Weber, Richard  
 APPLICANT: Bezabeh, Binyam  
 TITLE OF INVENTION: THEREOF  
 FILE REFERENCE: AGENIX\_051A  
 CURRENT APPLICATION NUMBER: US/10/041.860  
 NUMBER OF SEQ ID NOS: 377  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 288  
 LENGTH: 126  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-10-041-860-288

Query Match 88.3%; Score 593.5; DB 4; Length 126;  
 Best Local Similarity 89.7%; Pred. No. 1.3e-46;  
 Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;  
 Matches 113; Conservation 4; Mismatches 8; Indels 1; Gaps 1;

Qy 1 QVQLVQSAEVKKPGASVKSCKASGTTFTSDINWVQATQGGLEMMGWINPNSGNTDY 60  
 Db 1 QVQLVQSAEVKKPGASVKSCKASGTTFTSDINWVQATQGGLEMMGWINPNSGNTGY 60  
 Qy 61 AOKPQGRVTMTRDTISIATAYMELLSLRSEDTAIYCYVR-GFGYSYNYDYYGMDVNGQT 119  
 Db 61 AOKPQGRVTMTRNTISIATAYMELLSLRSEDTAIYCYVR-GFGYSYNYDYYGMDVNGQT 120

Qy 120 TVTVSS 125  
 Db 121 TVTVSS 126

RESULT 15  
 US-10-041-860-238  
 Sequence 238, Application US/10041860  
 Publication No. US20030157109A1  
 GENERAL INFORMATION  
 APPLICANT: Corvalan, Jose R.P.  
 APPLICANT: Jia, Xiao-Chi  
 APPLICANT: Feng, Xiao  
 APPLICANT: Yang, Xiao-Dong  
 APPLICANT: Chen, Francine  
 APPLICANT: Gazit, Gadi  
 APPLICANT: Weber, Richard  
 APPLICANT: Bezabeh, Binyam  
 TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES  
 FILE REFERENCE: AGENIX\_051A  
 CURRENT APPLICATION NUMBER: US/10/041.860  
 NUMBER OF SEQ ID NOS: 377  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 288  
 LENGTH: 126  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-10-041-860-238

Query Match 88.3%; Score 593.5; DB 4; Length 126;  
 Best Local Similarity 89.7%; Pred. No. 1.3e-46;  
 Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;  
 Matches 113; Conservation 4; Mismatches 8; Indels 1; Gaps 1;

Qy 1 QVQLVQSAEVKKPGASVKSCKASGTTFTSDINWVQATQGGLEMMGWINPNSGNTDY 60  
 Db 1 QVQLVQSAEVKKPGASVKSCKASGTTFTSDINWVQATQGGLEMMGWINPNSGNTGY 60  
 Qy 61 AOKPQGRVTMTRDTISIATAYMELLSLRSEDTAIYCYVR-GFGYSYNYDYYGMDVNGQT 119  
 Db 61 AOKPQGRVTMTRNTISIATAYMELLSLRSEDTAIYCYVR-GFGYSYNYDYYGMDVNGQT 120

Qy 120 TVTVSS 125  
 Db 121 TVTVSS 126

RESULT 14  
 US-10-665-383-18  
 Sequence 18, Application US/10665383  
 Publication No. US20040141963A1

Qy 4 LVQSGAEVKKPGASVKSCKASGTTFTSDINWVQATQGGLEMMGWINPNSGNTDYAQK 63  
 Db 3 LVQSGAEVKKPGASVKSCKASGTTFTSDINWVQATQGGLEMMGWINPNSGNTGYAQK 62  
 Qy 64 FGGRVTMTRDTISIATAYMELLSLRSEDTAIYCYVR-GFGYSYNYDYYGMDVNGQTVT 122

Db 63 FQGRVTMTRNTSISTAYMELSSLRSEDATVYYCAREGIAVAGTYYCNDVWGQGTTVT 122  
Qy 123 VSS 125  
Db 123 VSS 125

Search completed: May 15, 2006, 17:25:06  
Job time : 127.073 secs

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 15, 2006, 17:21:22 ; Search time 19.8498 Seconds  
 (without alignments)

295.651 Million cell updates/sec

Title: US-10-041-860-48  
 Perfect score: 672  
 Sequence: 1 QVQLVQSGAEVKKPGASVKKV.....YDYYGMDVWGQCTTVTVSS 125

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications AA\_New:  
 1: /SIDSS5/ptodata/1/pubpa/DS08 NEW PUB.PEP1:/\*  
 2: /SIDSS5/ptodata/1/pubpa/DS06 NEW PUB.PEP1:/\*  
 3: /SIDSS5/ptodata/1/pubpa/DS07 NEW PUB.PEP1:/\*  
 4: /SIDSS5/ptodata/1/pubpa/DS08 NEW PUB.PEP1:/\*  
 5: /SIDSS5/ptodata/1/pubpa/PCN\_NEW PUB.PEP1:/\*  
 6: /SIDSS5/ptodata/1/pubpa/DS09 NEW PUB.PEP1:/\*  
 7: /SIDSS5/ptodata/1/pubpa/DS10 NEW PUB.PEP1:/\*  
 8: /SIDSS5/ptodata/1/pubpa/DS11 NEW PUB.PEP1:/\*  
 9: /SIDSS5/ptodata/1/pubpa/DS10\_NEW PUB.PEP1:/\*  
 10: /SIDSS5/ptodata/1/pubpa/DS11\_NEW PUB.PEP1:/\*  
 11: /SIDSS5/ptodata/1/pubpa/DS11\_NEW PUB.PEP1:/\*  
 12: /SIDSS5/ptodata/1/pubpa/DS60\_NEW PUB.PEP1:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	561.5	83.6	122	9	US-10-082-440-61	Sequence 61, App1
2	558.5	83.1	145	9	US-10-721-763-29	Sequence 29, App1
3	541.5	81.3	124	11	US-11-040-159-8	Sequence 8, App1
4	541.5	80.6	120	9	US-10-334-397-36	Sequence 36, App1
5	541.5	80.6	120	9	US-10-834-397-59	Sequence 59, App1
6	536.5	79.8	247	11	US-11-514-515-1729	Sequence 1729, App1
7	536.5	79.8	247	11	US-11-266-444-1729	Sequence 1729, App1
8	536	79.8	125	9	US-10-382-440-45	Sequence 45, App1
9	534.5	79.5	249	11	US-11-054-515-919	Sequence 919, App1
10	534.5	79.5	249	11	US-11-266-444-919	Sequence 919, App1
11	528	78.6	117	9	US-10-834-397-22	Sequence 22, App1
12	527.5	78.5	122	10	US-11-211-917-110	Sequence 110, App1
13	524.5	78.1	245	11	US-11-054-515-1896	Sequence 1896, App1
14	524.5	78.1	245	11	US-11-266-444-1896	Sequence 1896, App1
15	524	78.0	255	11	US-11-054-515-1407	Sequence 1407, App1
16	524	78.0	255	11	US-11-266-444-1407	Sequence 1407, App1
17	523.5	77.9	247	11	US-11-054-515-927	Sequence 927, App1
18	523.5	77.9	247	11	US-11-054-515-948	Sequence 948, App1
19	523.5	77.9	247	11	US-11-266-444-927	Sequence 927, App1
20	523.5	77.9	247	11	US-11-266-444-948	Sequence 948, App1
21	520	77.4	256	11	US-11-054-515-1301	Sequence 1301, App1

## ALIGNMENTS

RESULT 1  
 US-10-982-440-61  
 ; Sequence 61, Application US/10982440  
 ; Publication No. US2006018909A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Oliner, John  
 ; INVENTION: Argioprotein-2 Specific Binding Agents  
 ; TITLE OF INVENTION: Argioprotein-2 Specific Binding Agents  
 ; FILE REFERENCE: 04-881-A  
 ; CURRENT APPLICATION NUMBER: US/10/982,440  
 ; CURRENT FILING DATE: 2004-11-04  
 ; PRIOR APPLICATION NUMBER: 60/620,161  
 ; PRIOR FILING DATE: 2004-10-19  
 ; NUMBER OF SEQ ID NOS: 215  
 ; SOFTWARE: Patentin version 3.3  
 ; SEQ ID NO: 61  
 ; LENGTH: 122  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-982-440-61

Query Match 83.6%; Score 561.5%; DB 9; Length 122;  
 Best Local Similarity 86.4%; pred. No. 2.3e-44; Mismatches 9; Indels 3; Gaps 1;

Qy 1 QVQLVSGAEYKKPGASVKKVSKASGYTFSYDINVRQATGQGLEWMGTPINPNSGNTYD 60  
 Db 1 QVQLVSGAEYKKPGASVKKVSKASGYTFSYDINVRQATGQGLEWMGTPINPNSGNTYD 60  
 Qy 61 AQKPGQRVTVTRDTSTISAYMELSLRSLSRDTAIIYVTVGRGFSYNTYYGMDVNGQGTT 120  
 Db 61 AQKPGQRVTVTRDTSTISAYMELSLRSLSRDTAIIYVTVGRGFSYNTYYGMDVNGQGTT 117  
 Qy 121 VTVSS 125  
 Db 118 VTVSS 122

RESULT 2  
 US-10-721-763-29  
 ; Sequence 29, Application US/10721763  
 ; Publication No. US2005249729A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIRIN BEER KABUSHIKI KAISHA

TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY  
FILE REFERENCE: PH-1573-PCT  
CURRENT APPLICATION NUMBER: US/10/721,763  
CURRENT FILING DATE: 2003-11-26  
PRIORITY APPLICATION NUMBER: JP2001-150213  
PRIOR FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: JP2001-243040  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: JP2001-314489  
PRIOR FILING DATE: 2001-10-11  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 29  
LENGTH: 145  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-721-763-29

Query Match 83.1%; Score 558.5%; DB 9; Length 145;  
Best Local Similarity 83.3%; Pred. No. 5.1e-44;  
Matches 105; Conservative 9; Mismatches 11; Indels 1; Gaps 1;  
Qy 1 QVQLVQSGAEVKPGASVKVSKCKASGYFTSYDINWROATGQLEWMGWINPNSGNTDY 60  
Db 20 QVQLVQSGAEVKPGASVKVSKCKASGYFTSYDINWROATGQLEWMGWINPNSGNTDY 79  
Qy 61 AQKFGQRTMTRDTISIATAYMELSSRSRDTAVYCAASGYTYYGMDWQGTT 119  
Db 80 PQKFGQRTMTRDTISIATAYMELSSRSRDTAVYCAASGYTYYGMDWQGTT 139  
Qy 120 TVTVSS 125  
Db 140 TVTVSS 145

RESULT 3  
US-11-040-159-8  
Sequence 8, Application US/11040159  
Publication No. US2005025552A1  
GENERAL INFORMATION:  
APPLICANT: Flynn, Peter  
APPLICANT: Luehrs, Kenneth  
APPLICANT: Balint, Robert F.  
APPLICANT: Her, Jeng Horng  
APPLICANT: Bebbington, Christopher R.  
APPLICANT: Yarranton, Geoffrey T.  
TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential  
TITLE OF INVENTION: Binding Determinants  
FILE REFERENCE: 021167-001730US  
CURRENT FILING DATE: 2005-01-20  
PRIOR FILING DATE: 2004-01-20  
PRIOR APPLICATION NUMBER: US 60/537,364  
PRIOR FILING DATE: 2004-02-23  
NUMBER OF SEQ ID NOS: 133  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 8  
LENGTH: 124  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: OTHER INFORMATION: Description of Artificial Sequence:BA130-5-E10 Vh human  
OTHER INFORMATION: variable region containing minimal essential binding  
OTHER INFORMATION: specificity domain (MEB3D) in heavy chain CDR3 from murine  
OTHER INFORMATION: anti-PcrV antibody M166 and complete human J-region (JH6)  
US-11-040-159-8

Qy 1 QVQLVQSGAEVKPGASVKVSKCKASGYFTSYDINWROATGQLEWMGWINPNSGNTDY 60  
Db 1 EVQLVQSGAEVKPGASVKVSKCKASGYFTSYDINWROATGQLEWMGWINPNSGNTDY 60  
Qy 61 AQKFGQRTMTRDTISIATAYMELSSRSRDTAVYCAASGYTYYGMDWQGTT 120  
Db 61 AQKFGQRTMTRDTISIATAYMELSSRSRDTAVYCAASGYTYYGMDWQGTT 119  
Qy 121 TVTVSS 125  
Db 120 TVTVSS 124

RESULT 4  
US-10-834-397-36  
Sequence 36, Application US/10834397  
Publication No. US2006000334A1  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Tilg, Vic  
Ge, Liming  
Moroney, Simon  
Blueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly) peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESS: James P. Haley, Jr., Eqd. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.3.0 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/834,397  
FILING DATE: 29-Apr-2004  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,324  
FILING DATE: 24-Jan-2000  
APPLICATION NUMBER: US/09/025,769  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: BP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James P. Haley, Jr., Eqd.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-10-834-397-36

Qy 1 QVQLVQSGAEVKPGASVKVSKCKASGYFTSYDINWROATGQLEWMGWINPNSGNTDY 60  
Db 1 QVQLVQSGAEVKPGASVKVSKCKASGYFTSYDINWROATGQLEWMGWINPNSGNTDY 60

Qy 61 AOKFOGRVTTMRTDTISIATAYMELSSLRSEDATAIYCVRGFGSYNDDYGMNDVNGQGTT 120  
 Db 61 AOKFOGRVTTMRTDTISIATAYMELSSLRSEDATAIYCVRGFGSYNDDYGMNDVNGQGTT 115

Qy 121 VTVSS 125  
 Db 116 VTVSS 120

RESULT 5  
 US-10-834-397-59  
 Sequence 59, Application US/10834397  
 Publication No. US2006000333411  
 GENERAL INFORMATION:  
 APPLICANT: Knappik, Achim  
 Pack, Peter  
 Ilag, Vic  
 Ge, Liming  
 Moroney, Simon  
 Pluckthun, Andreas  
 TITLE OF INVENTION: Protein(Poly)peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10021  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentn Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/834,397  
 FILING DATE: 29-Apr-2004  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/490,324  
 FILING DATE: 24-Jan-2000  
 APPLICATION NUMBER: US/09/025,769  
 FILING DATE: 18-FEB-1998  
 APPLICATION NUMBER: EP 95 11 3021.0  
 ATTORNEY/AGENT INFORMATION:  
 NAME: James F. Haley, Jr., Esq.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: MORPHO/5  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)596-9000  
 TELEFAX: (212)596-9090  
 INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 120 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
 us-10-834-397-59

Query Match 80.6%; Score 541.5; DB 9; Length 120;  
 Best Local Similarity 84.0%; Pred. No. 1.5e-42;  
 Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

Qy 1 OYOLVQSAEVKPGASVVKVSKCKASGTYTSTDINVYRQATSGQGLEWMQWNPNSGNTDY 60  
 Db 1 OYOLVQSAEVKPGASVVKVSKCKASGTYTSTDINVYRQATSGQGLEWMQWNPNSGNTDY 60

Qy 61 AOKFOGRVTTMRTDTISIATAYMELSSLRSEDATAIYCVRGFGSYNDDYGMNDVNGQGTT 120  
 Db 61 AOKFOGRVTTMRTDTISIATAYMELSSLRSEDATAIYCVRGFGSYNDDYGMNDVNGQGTT 115

Qy 121 VTVSS 125

RESULT 6  
 US-11-054-515-1729  
 Sequence 1729, Application US/11054515  
 Publication No. US200505532A1  
 GENERAL INFORMATION:  
 APPLICANT: Ruben et al.  
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
 FILE REFERENCE: PFS23P3  
 CURRENT APPLICATION NUMBER: US/11/054,515  
 PRIOR APPLICATION NUMBER: 2005-02-10  
 PRIOR FILING DATE: 2004-02-11  
 PRIOR APPLICATION NUMBER: 60/543,296  
 PRIOR FILING DATE: 2004-06-18  
 PRIOR APPLICATION NUMBER: 10/293,418  
 PRIOR FILING DATE: 2002-11-14  
 PRIOR APPLICATION NUMBER: 60/331,469  
 PRIOR FILING DATE: 2001-11-16  
 PRIOR APPLICATION NUMBER: 60/340,817  
 PRIOR FILING DATE: 2001-12-19  
 PRIOR APPLICATION NUMBER: 09/880,748  
 PRIOR FILING DATE: 2001-06-15  
 PRIOR APPLICATION NUMBER: 60/293,499  
 PRIOR FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: 60/277,379  
 PRIOR FILING DATE: 2001-03-21  
 PRIOR APPLICATION NUMBER: 60/276,248  
 PRIOR FILING DATE: 2001-03-16  
 PRIOR APPLICATION NUMBER: 60/240,816  
 PRIOR FILING DATE: 2000-10-17  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 3247  
 SEQ ID NO: 1729  
 LENGTH: 247  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-054-515-1729

Query Match 79.8%; Score 536.5; DB 11; Length 247;  
 Best Local Similarity 81.6%; Pred. No. 8.7e-42;  
 Matches 102; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 OYOLVQSAEVKPGASVVKVSKCKASGTYTSTDINVYRQATSGQGLEWMQWNPNSGNTDY 60  
 Db 1 OYOLVQSAEVKPGASVVKVSKCKASGTYTSTDINVYRQATSGQGLEWMQWNPNSGNTDY 60

Qy 61 AQKPFQGRVTTMRTDTISIATAYMELSSLRSEDATAIYCVRGFGSYNDDYGMNDVNGQGTT 120  
 Db 61 AQKPFQGRVTTMRTDTISIATAYMELSSLRSEDATAIYCVRGFGSYNDDYGMNDVNGQGTT 119

Qy 121 VTVSS 125  
 Db 120 VTVSS 124

RESULT 7  
 US-11-266-444-1729  
 Sequence 1729, Application US/11266444  
 Publication No. US20060062789A1  
 GENERAL INFORMATION:  
 APPLICANT: Ruben et al.  
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat

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; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/216,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1729
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1729

Query Match 79.8%; Score 536.5; DB 11; Length 247;
Best Local Similarity 81.6%; Pred. No. 8.7e-42;
Matches 102; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
Qy 1 QVQLVSGAELYKPGASVKVSKASGYFTSYDINVRQATGQLEWMGINPNSGNTD 60
Db 1 QVQLVSGAELYKPGASVKVSKASGYFTSYDINVRQATGQLEWMGINPNSGNTD 60

Qy 61 AOKPQGRVMTRDTIS1STAYMELSLRSRDTAIVYCVRGFGSYNDDYTGMDWQGQTT 120
Db 61 AOKPQGRVMTRDTIS1STAYMELSLRSRDTAIVYCVRGFGSYNDDYTGMDWQGQTT 119

Qy 121 VTVSS 125
Db 120 VTVSS 124

RESULT 8
US-10-982-440-45
; Sequence 45, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
; APPLICANT: Oliver, John
; APPLICANT: Graham, Kevin
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; FILE REFERENCE: 04-981-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/620,161
; PRIOR FILING DATE: 2004-10-19
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 45
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-440-45

Query Match 79.8%; Score 536; DB 9; Length 125;
Best Local Similarity 81.6%; Pred. No. 4.9e-42;
Matches 102; Conservative 7; Mismatches 16; Indels 0; Gaps 0;
Qy 1 QVQLVSGAELYKPGASVKVSKASGYFTSYDINVRQATGQLEWMGINPNSGNTD 60
Db 1 QVQLVSGAELYKPGASVKVSKASGYFTSYDINVRQATGQLEWMGINPNSGNTD 60

Qy 61 AOKPQGRVMTRDTIS1STAYMELSLRSRDTAIVYCVRGFGSYNDDYTGMDWQGQTT 120
Db 61 AOKPQGRVMTRDTIS1STAYMELSLRSRDTAIVYCVRGFGSYNDDYTGMDWQGQTT 120

Qy 121 VTVSS 125
Db 121 VTVSS 125

RESULT 9
US-11-054-515-919
; Sequence 919, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulatory Proteins
; FILE REFERENCE: PFS23P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-22

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PRIOR APPLICATION NUMBER: 60/293,499  
 PRIOR FILING DATE: 2001-05-25  
 NUMBER OF SEQ ID NOS: 3239  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 919  
 LENGTH: 249  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-266-444-919

Query Match Similarity 79.5%; Score 534.5; DB 11; Length 249;  
 Best Local Similarity 81.7%; Pred. No. 1..3e-41;  
 Matches 103; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 QVQLVQSGAEVVKPGASVKVSKASCGTPTSDINWVQATQGGLEMWGWINPNSGNTDY 60  
 Db 1 AQKPGQRTVMTRDTSISTAYMELSSRSEDTAYCVRGFSYNTD-YGMDWQGQT 60

Qy 61 AQKPGQRTVMTRDTSISTAYMELSSRSEDTAYCVRGFSYNTD-YGMDWQGQT 119  
 Db 61 AQKPGQRTVMTRDTSISTAYMELSSRSEDTAYCVRGFSYNTD-YGMDWQGQT 120

Qy 120 TVTVSS 125  
 Db 121 TVTVSS 126

RESULT 11  
 US-11-211-917-110  
 ; Sequence 110, Application US/11211917  
 ; Publication No. US200601093600A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BEDIAN, VAHE  
 ; GLADIAN, RONALD P.  
 ; CORVALAN, JOSE  
 ; JIA, XIAO-CHI  
 ; FENG, XIAO  
 ; TITLE OF INVENTION: ANTIBODIES TO CD40  
 ; FILE REFERENCE: ABX-PP/3 US  
 ; CURRENT APPLICATION NUMBER: US/11/211,917  
 ; PRIORITY APPLICATION NUMBER: 60/348,980  
 ; PRIOR FILING DATE: 2005-08-25  
 ; PRIOR APPLICATION NUMBER: US/10/292,088  
 ; NUMBER OF SEQ ID NOS: 147  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 110  
 ; LENGTH: 122  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-211-917-110

RESULT 11  
 US-10-834-397-22  
 ; Sequence 22, Application US/10834397  
 ; Publication No. US20060003334A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Knappik, Achim  
 ; Pack, Peter  
 ; Ilag, Vic  
 ; Ge, Liming  
 ; Moroney, Simon  
 ; Plueckthun, Simon Andreas  
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 ; NUMBER OF SEQUENCES: 373  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEES: James F. Haley, Jr., Esq. c/o Fish & Neave  
 ; STREET: 1251 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10021  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/834,397  
 ; FILING DATE: 29-Apr-2004  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/490,324  
 ; FILING DATE: 24-Jan-2000  
 ; APPLICATION NUMBER: US/09/025,769  
 ; FILING DATE: 18-FEB-1998  
 ; APPLICATION NUMBER: EP 95 11 3021.0  
 ; FILING DATE: 18-AUG-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: James F. Haley, Jr., Esq.  
 ; REGISTRATION NUMBER: 27,794  
 ; REFERENCE/DOCKET NUMBER: MORPHO/5  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212)596-9000  
 ; TELEFAX: (212)596-9090  
 ; INFORMATION FOR SEQ ID NO: 22:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 117 amino acids  
 ; TYPE: amino acid

Query Match Similarity 78.6%; Score 528; DB 9; Length 117;  
 Best Local Similarity 82.5%; Pred. No. 2.5e-41;  
 Matches 104; Conservative 5; Mismatches 7; Indels 10; Gaps 2;

Qy 1 QVQLVQSGAEVVKPGASVKVSKASCGTPTSDINWVQATQGGLEMWGWINPNSGNTDY 60  
 Db 1 QVQLVQSGAEVVKPGASVKVSKASCGTPTSDINWVQATQGGLEMWGWINPNSGNTDY 60

Qy 61 AQKPGQRTVMTRDTSISTAYMELSSRSEDTAYCVR-GFGYSNYDYYGMDWQGQT 119  
 Db 61 AQKPGQRTVMTRDTSISTAYMELSSRSEDTAYCVR-GFGYSNYDYYGMDWQGQT 111

RESULT 12  
 US-11-211-917-110  
 ; Sequence 110, Application US/11211917  
 ; Publication No. US200601093600A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BEDIAN, VAHE  
 ; GLADIAN, RONALD P.  
 ; CORVALAN, JOSE  
 ; JIA, XIAO-CHI  
 ; FENG, XIAO  
 ; TITLE OF INVENTION: ANTIBODIES TO CD40  
 ; FILE REFERENCE: ABX-PP/3 US  
 ; CURRENT APPLICATION NUMBER: US/11/211,917  
 ; PRIORITY APPLICATION NUMBER: 60/348,980  
 ; PRIOR FILING DATE: 2005-08-25  
 ; PRIOR APPLICATION NUMBER: US/10/292,088  
 ; NUMBER OF SEQ ID NOS: 147  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 110  
 ; LENGTH: 122  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-211-917-110

Query Match Similarity 78.5%; Score 527.5; DB 10; Length 122;  
 Best Local Similarity 79.4%; Pred. No. 2.9e-41;  
 Matches 102; Conservative 7; Mismatches 10; Indels 9; Gaps 2;

Qy 1 QVQLVQSGAEVVKPGASVKVSKASCGTPTSDINWVQATQGGLEMWGWINPNSGNTDY 60  
 Db 1 QVQLVQSGAEVVKPGASVKVSKASCGTPTSDINWVQATQGGLEMWGWINPNSGNTDY 60

Qy 61 AQKPGQRTVMTRDTSISTAYMELSSRSEDTAYCVR-GFSYNTDYYGMDWQGQT 117  
 Db 61 AQKPGQRTVMTRDTSISTAYMELSSRSDDTAVYCARGYCTNGCYFDY----WQG 114

RESULT 13  
 US-11-054-515-1896  
 ; Sequence 1896, Application US/11054515  
 ; Publication No. US2005025532A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

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; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1896

Query Match 78.1%; Score 524.5; DB 11; Length 245;
Best Local Similarity 81.7%; Pred. No. 1.1e-40;
Matches 103; Conservative 6; Mismatches 10; Indels 8; Gaps 2;

Qy 1 QVQLYSGAELYKKPGASVKYSCKASQSYTFTSYDINWVQATGQHLFWMGWNPNSGNTDY 60
Db 1 QVQLYSGAELYKKPGASVKYSCKASQSYTFTSYDINWVQATGQHLFWMGWNPNSGNTDY 60

Qy 61 AQQFQGRVITRDTTSIATAYMELSSRSEDTAIYCVR-GFGYSYNTYXGMDWVGQGT 119
Db 61 SQKFQGRVITRDTTSIATAYMELSSRSEDTAIYCVR-GFGYSYNTYXGMDWVGQGT 114

Qy 120 TVTVSS 125
Db 115 MVTVSS 120

RESULT 15
US-11-054-515-1407
Sequence 1407, Application US/11054515
; Publication No. US20050255532A1
; PUBLIC INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: EP52393
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO: 1407
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1407

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Db 116 ||||:||||| MDVWGKGTMTVSS 129

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Job time : 20.8498 secs

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GenCore version 5.1.8  
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run on: May 15, 2006, 16:59:17 ; Search time 25:2146 Seconds  
 (without alignments)  
 479.989 Million cell updates/sec

title: US-10-041-860-48  
 perfect score: 672  
 sequence: 1 QVQVQSGAEVKPGASVVKV.....YDYYGMDVWGQGTTVYSS 125

scoring table: BLOSUM62

searched: 283416 seqs, 96216763 residues

minimum DB seq length: 0  
maximum DB seq length: 2000000000  
post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

database : BTB 80:\*

Piracy 11

3: pir3:\*

ered. No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, and is decided by a random draw of the total number of results.

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result	No.	Score	Query	Length	DB	ID	Description
1	557	82.9	S34014	127	2	S34014	Ig heavy chain V r
2	537.5	80.0	S31600	136	2	S31600	Ig heavy chain V r
3	534	79.5	S44393	129	2	S44393	Ig heavy chain V r
4	516.5	76.9	S36265	118	2	S36265	Ig heavy chain V r
5	515	76.6	D31548	123	2	D31548	Ig heavy chain V r
6	514	76.5	S32660	129	2	S32660	Ig heavy chain V r
7	511.5	76.1	S4530	135	2	S4530	Ig heavy chain V r
8	510.5	76.0	S31596	132	2	S31596	Ig heavy chain V r
9	500	74.4	S26792	131	2	S26792	Ig heavy chain V r
10	499	74.3	PR0961	119	2	PR0961	Ig heavy chain V r
11	496.5	73.9	PH1670	110	2	PH1670	Ig heavy chain V r
12	496	73.8	S26918	98	2	S26918	Ig heavy chain V r
13	495.5	73.7	PR0954	132	2	PR0954	Ig heavy chain V r
14	495.5	73.7	S21623	171	2	S21623	Ig heavy chain V r
15	494.5	73.6	PH1666	118	2	PH1666	Ig heavy chain V r
16	493.5	73.4	PR0960	136	2	PR0960	Ig heavy chain V r
17	488.5	72.7	B1HUND	143	1	B1HUND	Ig heavy chain pre
18	488	72.6	PH0955	127	2	PH0955	Ig heavy chain V r
19	487.5	72.5	S19665	124	2	S19665	Ig heavy chain V r
20	486	72.3	C31548	133	2	C31548	Ig heavy chain V-1
21	486	72.3	S14683	627	2	S14683	Ig mu chain precur
22	484	72.0	A31483	142	2	A31483	Ig heavy chain V r
23	480	71.4	S36271	122	2	S36271	Ig heavy chain V r
24	480	71.4	PL0105	160	2	PL0105	anti-Pk2 erythrocy
25	477.5	71.1	B33548	126	2	B33548	Ig heavy chain V-1
26	476.5	70.9	PH1667	114	2	PH1667	Ig heavy chain V r
27	473.5	70.5	PR0952	128	2	PR0952	Ig heavy chain V r
28	472	70.3	S31999	120	2	S31999	Ig heavy chain V r
29	468	69.6	PR6668	109	2	PR6668	Ig heavy chain V r

C;Keywords: heterotetramer; immunoglobulin homology <IMM>  
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match Score 537.5; DB 2; Length 136;  
 Best Local Similarity 80.0%; Pred. No. 8 1e-41;  
 Matches 103; Conservative 6; Mismatches 7; Indels 9; Gaps 1;

Qy 1 QVQLVSGAELYKPGASVKVSKASGYFTSYDINVRQATGQGLEWMGWINPNSGNTDY 60  
 Db 20 QVQLVSGAELYKPGASVKVSKASGYFTSYDINVRQATGQGLEWMGWINPNSGNTDY 79

Qy 61 AQKFGQRTVMTRDTISIATYMEPLLSSRLSRTDAIYCYCVRGFSYNTDYYGMDVQGQTT 120  
 Db 80 AQKFGQRTVMTRDTISIATYMEPLLSSRLSRTDAIYCYCVRGFSYNTDYYGMDVQGQTT 130

Qy 121 VTVSS 125  
 Db 131 VTVSS 135

RESULT 3  
 S4 6393  
 Ig heavy chain V region - human  
 C;Species: Homo sapiens (man)  
 C;Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
 C;Accession: S46393  
 R;Pigini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.  
 J. Mol. Biol. 239, 68-78, 1994  
 A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by  
 A;Reference number: S46390; MUID:94254092; PMID:8196048  
 A;Accession: S46393  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-129 <GTR>  
 A;Cross-references: UNIPARC:UPI000011663A; EMBL:231680; PIDN:CAA83485.1; PI  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin homology <IMM>  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match Score 534; DB 2; Length 129;  
 Best Local Similarity 79.0%; Pred. No. 1.6e-40;  
 Matches 103; Conservative 7; Mismatches 15; Indels 4; Gaps 1;

Qy 1 QVQLVSGAELYKPGASVKVSKASGYFTSYDINVRQATGQGLEWMGWINPNSGNTDY 60  
 Db 1 QVQLVSGAELYKPGASVKVSKASGYFTSYDINVRQATGQGLEWMGWINPNSGNTDY 60

Qy 61 AQKFGQRTVMTRDTISIATYMEPLLSSRLSRTDAIYCYCVRGFSYNTDYYGMDVQGQTT 116  
 Db 61 AQKFGQRTVMTRDTISIATYMEPLLSSRLSRTDAIYCYCVRGFSYNTDYYGMDVQGQTT 120

Qy 117 QGTTVTVSS 125  
 Db 121 KGTTVTVSS 129

RESULT 4  
 S3 6265  
 Ig heavy chain V region (clone alpha-MUCL-1) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
 C;Accession: S36265  
 R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Embleton, M.J.; McCafferty, J.  
 EMBO J. 12, 725-734, 1993  
 A;Title: Human anti-self antibodies with high specificity from phage display libraries.  
 A;Reference number: S36256; MUID:93178448; PMID:7679990  
 A;Accession: S36265  
 A;Status: preliminary; nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-129 <GTR>  
 A;Cross-references: UNIPARC:UPI00001180BB; EMBL:218851; MUID:933124; PIDN:CAA79303.1; PID  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin homology <IMM>  
 F;15-98/Domain: immunoglobulin homology <IMM>

RESULT 5  
 D33548  
 Ig heavy chain V-1 region (WIL2) - human  
 C;Species: Homo sapiens (man)  
 C;Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996  
 C;Accession: D33548  
 R;Klappa, T.J.; Tomhave, B.; Pratt, L.P.; Duffy, S.; Chen, P.P.; Carson, D.A.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989  
 A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr  
 A;Reference number: A33548; MUID:934575; PMID:1503826  
 A;Accession: D33548  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra.  
 A;Molecule type: mRNA  
 A;Residues: 1-123 <GTR>  
 A;Cross-references: UNIPARC:UPI0000176909  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match Score 515; DB 2; Length 123;  
 Best Local Similarity 78.6%; Pred. No. 7.2e-39;  
 Matches 99; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

Qy 1 QVQLVSGAELYKPGASVKVSKASGYFTSYDINVRQATGQGLEWMGWINPNSGNTDY 60  
 Db 1 QVQLVSGAELYKPGASVKVSKASGYFTSYDINVRQATGQGLEWMGWINPNSGNTDY 60

Qy 61 AQKFGQRTVMTRDTISIATYMEPLLSSRLSRTDAIYCYCVRGFSYNTDYYGMDVQGQTT 119  
 Db 61 AQKFGQRTVMTRDTISIATYMEPLLSSRLSRTDAIYCYCVRGFSYNTDYYGMDVQGQTT 117

Qy 120 VTVSS 125  
 Db 118 VTVSS 123

RESULT 6  
 S36260  
 Ig heavy chain V regions (clone alpha-CRA4-8A) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
 C;Accession: S36260  
 R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Embleton, M.J.; McCafferty, J.  
 EMBO J. 12, 725-734, 1993  
 A;Title: Human anti-self antibodies with high specificity from phage display libraries.  
 A;Reference number: S36256; MUID:93178448; PMID:7679990  
 A;Accession: S36260  
 A;Status: preliminary; nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-129 <GTR>  
 A;Cross-references: UNIPARC:UPI00001180BB; EMBL:218851; MUID:933124; PIDN:CAA79303.1; PID  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 514; DB 2; Length 129;  
 Best Local Similarity 78.3%; Prod. No. 9.3e-39; Indels 4; Gaps 2;  
 Matches 101; Conservative 8; Mismatches 16; Indels 4; Gaps 2;

Qy 1 QVOLVQSAEVKPGASVKVSCKASCGTPTSDINWYRQATQGLEMGWNPNSGNTY 60  
 Db 1 QVOLQSQSAEVKPGASVKVSCKASCGTPTSDINWYRQATQGLEMGWNPNSGNTY 60

Qy 61 AOKPQGRVTMTRDTISIAYMELSLRSSEDTAIYCYRGFISYNTDYYGMDVWGGTT 120  
 Db 61 AOKPQGRVTMTRDTISIAYMELSLRSSEDTAIYCYRGFISYNTDYYGMDVWGGTT 120

Qy 117 QGTTVTVSS 125  
 Db 121 KGTTVTVSS 129

RESULT 9  
 S26792  
 Ig heavy chain V region - human  
 C;Species: Homo sapiens (man)  
 C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
 C;Accession: S26792  
 R;Mortari, P.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.  
 R;J. Immunol. 22, 241-245, 1992  
 A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam  
 A;Reference number: S26786; PMID:92111632; PMID:1730251  
 A;Accession: S26792  
 A;Status: Preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-131 <MOR>  
 A;Cross-references: UNIPARC:UPI0000115FC3; ENBL:X61012; PIDN:932804; PMID:443346.1; PI  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-38/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 500; DB 2; Length 131;  
 Best Local Similarity 72.5%; Prod. No. 1.6e-37;  
 Matches 95; Conservative 13; Mismatches 17; Indels 6; Gaps 2;

Qy 1 QVOLVQSAEVKPGASVKVSCKASCGTPTSDINWYRQATQGLEMGWNPNSGNTY 60  
 Db 1 QVOLVQSGSEELKKPGASVKVSCKASCGTPTSDINWYRQATQGLEMGWNPNSGNTY 60

Qy 61 AOKPQGRVTMTRDTISIAYMELSLRSSEDTAIYCYRGFISYNTDYYGMDVWGGTT 114  
 Db 61 AQGFTGRFVSELDTSVSTAYLQISSLKAEDTAVYYCARATGNY --- NYDYYGMDV 114

Qy 115 WGQTTVTVSS 125  
 Db 121 WGKGTIVTVSS 131

RESULT 10  
 PH0961  
 Ig heavy chain V region (G6+ T-L33) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
 C;Accession: PH0961  
 R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
 J. Exp. Med. 175, 983-991, 1992  
 A;Title: Evidence for somatic selection of natural autoantibodies.  
 A;Reference number: PH0952; PMID:9220280; PMID:1552291  
 A;Accession: PH0961  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: DNA  
 A;Residues: 1-19 <MAR>  
 A;Cross-references: UNIPARC:UPI0000176C85  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;1-30/Region: framework 1  
 F;15-98/Region: immunoglobulin homology <IMM>  
 F;31-51/Region: complementarity-determining 1  
 F;36-50/Region: framework 2

Query Match 76.0%; Score 510.5; DB 2; Length 132;

RESULT 8  
 S31596  
 Ig heavy chain V region - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C;Accession: S31596  
 R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
 Submitted to the EMBL Data Library, June 1992  
 A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
 A;Reference number: S31585  
 A;Accession: S31596  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-132 <CJL>  
 A;Cross-references: UNIPARC:UPI0000116454; ENBL:Z14166; PIDN:930996; PMID:CAA78535.1; PI  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;34-117/Region: immunoglobulin homology <IMM>

PF51-67/Region: complementarity-determining 2	Query Match 74.3%; Score 499; DB 2; Length 119;
PF68-98/Region: framework 3	Best Local Similarity 79.2%; Pred. No. 1. 9e-37;
PF99-107/Region: complementarity-determining 3	Matches 99; Conservative 6; Mismatches 14; Indels 6; Gaps 1;
	Qy 1 QVQLQSGAERVKPGASVYKVSCKASGTYFTSYDINMYRQATQGLEMKGWINPNSGNTDY 60 Dbs 1 QVQLQSGAERVKPGASVYKVSCKASGTYFTSYDINMYRQATQGLEMKGWINPNSGNTDY 60
	Qy 61 AQRQFGRVITMTRDTSISTAYMELSLRSRSDTAYIYCYRQFGSYNTDYYGMDVWGQTT 120 Dbs 61 AQRQFGRVITADETSISTAYMELSLRSRSDTAYIYCYRQFGSYNTDYYGMDVWGQTT 114
	Qy 121 VTVSS 125 Dbs 115 VTVSS 119
<b>RESULT 11</b>	
	PH1670 Ig heavy chain V region (clone 2A12) - human (fragment)
	C:Species: Homo sapiens (man)
	C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
	C:Accession: PH1670
	C:Author: R.Hillson, J.L.; Karr, N.S.; Oppiger, I.R.; Mannik, M.; Sasso, E.H.
	C:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal A1 protein
	C:Reference number: PH1642; PMID:93301610; PMID:8315388
	C:Accession: PH1670
	A:Residues: 1-110 <HIL>
	A:Cross-references: UNIPARC:UPI0000176BEB
	A:Experimental source: B cell
	C:Superfamily: immunoglobulin V region; immunoglobulin homology
	C:Keywords: heterotetramer; immunoglobulin
	F:7-90/Domain: immunoglobulin homology <IMM>
	Query Match 73.9%; Score 496.5; DB 2; Length 110;
	Best Local Similarity 82.1%; Pred. No. 2. 3e-37;
	Matches 96; Conservative 6; Mismatches 8; Indels 7; Gaps 2;
	Qy 9 AERVKPGASVYKVSCKASGTYFTSYDINMYRQATQGLEMKGWINPNSGNTDYAQKFQGRV 68 Dbs 1 AERVKPGASVYKVSCKASGTYFTSYDINMYRQATQGLEMKGWINPNSGNTDYAQKFQGRV 60
	Qy 69 TMTRDTTSISTAYMELSLRSRSDTAYIYCYRQFGSYNTDYYGMDVWGQTTVYSS 125 Dbs 61 TMTRNTTSISTAYMELSLRSRSDTAYIYCYRQFGSYNTDYYGMDVWGQTTVYSS 110
<b>RESULT 12</b>	
	S26918 Ig heavy chain V region (DP-15) - human (fragment)
	C:Species: Homo sapiens (man)
	C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
	C:Accession: S26918
	C:Author: R.R.Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
	C:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of variable genes
	C:Reference number: S26885; PMID:9302117; PMID:1404388
	C:Accession: S26918
	A:Status: Preliminary
	A:Molecule type: DNA
	A:Residues: <TOM> 1-98
	A:Cross-references: UNIPARC:UPI000031F36; EMBL:Z12317; NID:932857; PIDN:CAA78187.1; PIDN:CAA78187.2
	C:Superfamily: immunoglobulin V region; immunoglobulin homology
	C:Keywords: heterotetramer; immunoglobulin
	F:7-98/Domain: immunoglobulin homology <IMM>
	Qy 72 9%; Score 496; DB 2; Length 98;

Query Match      73.7%;    Score 495.5;    DB 2;    Length 171;  
 Best Local Similarity      70.9%;    Pred. No. 5.5e-37;    Gaps 2;  
 Matches 95;    Conservative 9;    Mismatches 13;    Indels 17;    Gaps 2;

Qy      1 QVQLVQSGAEVKKPQGASVKVSCKASGYTFSYDINWVQATQGQLEMGWIPNSGNTDY 60  
 Db      20 QVQLVQSGAEVKKPQGASVKVSCKASGYTFSYDINWVQATQGQLEMGWIPNSGNTDY 79

Qy      61 AQQFQGRVTTMTRDTISIATAYMELLSLSRBDTALIYCYRGFGSYNTDYYG----- 111  
 Db      80 GQRFQGRVTTMTRDTISIATAYMELSLTSDDTAVYYCA-----1EYFYDSDLKPSDV 131

Qy      112 MDYWQGQTTVTVSS 125

Db      132 PDIWQGTTVTVSS 145

## RESULT 15

PH1666  
 19 heavy chain V region (clone 6C9) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
 C;Accession: PH1666  
 R;Hillson, J.L.; Karr, N.S.; Oppiger, I.R.; Mannik, M.; Sasso, B.H.  
 J;Exp. Med. 178, 331-336, 1993  
 A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A  
 A;Reference number: PH1642; MUID:93301610; PMID:8315388  
 A;Accession: PH1666  
 A;Molecule type: mRNA  
 A;Residues: 1-118 <HIL>  
 A;Cross-references: UNIPARC:UPI0000176BE7  
 A;Experimental source: B cell  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 P;7-90/Domain: immunoglobulin homology <IMM>  
 C;Keywords: heterotetramer; immunoglobulin  
 P;7-90/Domain: immunoglobulin homology <IMM>

Query Match      73.6%;    Score 494.5;    DB 2;    Length 118;  
 Best Local Similarity      80.5%;    Pred. No. 4.5e-37;    Gaps 1;  
 Matches 95;    Conservative 6;    Mismatches 16;    Indels 1;    Gaps 1;

Qy      9 AEVKKPGASVKVSCKASGYTFSYDINWVQATQGQLEMGWIPNSGNTDYAQKFQGRV 68  
 Db      1 AEVKKPGASVKVSCKASGYTFSYDINWVQATQGQLEMGWIPNSGNTDYAQKFQGRV 60

Qy      69 TMTRDTISIATAYMELLSLSSRDTAIIYCYRGFGSYNTDYYGMDWQGTTVTVSS 125  
 Db      61 TITRDTISAASTATMELSSRDTAIIYCYRGFGSYNTDYYGMDWQGTTVTVSS 118

Search completed: May 15, 2006, 17:04:50  
 Job time : 26.2146 sec

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RESULT 1						
Q96Q80 HUMAN				PRT; 159 AA.		
ID	Q96Q80_HUMAN	PRELIMINARY;				
AC	Q96Q80;					
DT	01-DEC-2001 (TREMBLrel. 19, Created)					
DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)					
DR	01-OCT-2003 (TREMBLrel. 25, Last annotation update)					
DB	Putative matrix cell adhesion molecule-3.					
OS	Homo sapiens (Human)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.					
OC	Q96Q80 rattus norvegicus					
OC	Q924Q6 mus musculus					
OC	Q924Q5 mus musculus					
OC	Q924Q3 mus musculus					
OC	Q924R1 mus musculus					
OC	P01747 mus musculus					
OC	Q924W9 mus musculus					
OC	Q924Q5 mus musculus					
OC	Q924R3 mus musculus					
OC	Q8Vcrx7 mus musculus					
OC	Q65Zr6 mus musculus					
OC	Q924Q9 mus musculus					
OC	Q924R0 mus musculus					
OC	Q6PjB2 mus musculus					
ALIGNMENTS						
SEARCHED						
2166443 seqs, 705528306 residues						
TOTAL NUMBER OF HITS SATISFYING CHOSEN PARAMETERS:						
2166443						
SEARCH						
Minimum DB seq length: 0						
Maximum DB seq length: 20000000000						
FIRST-PROCESSING: Minimum Match 0%						
Maximum Match 100%						
Listing First 45 summaries						
DATABASE :						
UniProt 05.80.*:						
1: uniprot_sprot;*						
2: uniprot_trembl;*						
PRED. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
1	497.5	74.0	159	2	Q96Q80_HUMAN	Q96Q80 homo sapien
2	494	73.5	119	2	Q96Q80_HUMAN	Q9u194 homo sapien
3	494	73.5	125	2	Q9uL95_HUMAN	Q9u195 homo sapien
4	491	73.1	244	2	Q65ZC8_HUMAN	Q65ZC8 homo sapien
5	488	72.7	147	1	Q9uLIC_HUMAN	P01744 homo sapien
6	481.5	71.7	124	2	Q9uL92_HUMAN	Q9u192 homo sapien
7	478.5	71.2	498	2	Q6u041_HUMAN	Q6n041 homo sapien
8	474	70.5	497	2	Q8VY24_HUMAN	Q8wy24 homo sapien
9	470.5	70.0	500	2	Q8RV0_HUMAN	Q9brv0 homo sapien
10	457.5	68.1	518	2	Q6uN00_HUMAN	Q6n030 homo sapien
11	455	67.7	119	2	Q9cY2Z_HUMAN	Q9yzz2 mus musculus
12	446	66.4	500	2	Q6uN91_HUMAN	Q6n091 homo sapien
13	441	65.6	117	1	Q8VY24_HUMAN	P23083 homo sapien
14	440	65.5	117	1	Q8VY24_HUMAN	P01743 homo sapien
15	438	65.2	480	2	Q6p089_HUMAN	Q6p089 homo sapien
16	436	64.9	458	2	Q5B022_RAT	Q5bjzz rattus norvegicus
17	433.5	64.5	469	2	Q7z7P5_HUMAN	Q7z7P5 homo sapien
18	430	64.0	481	2	Q91WT1_HUMAN	Q91wt1 mus musculus
19	429.5	63.9	116	2	Q9uL89_HUMAN	Q9u189 homo sapien
20	425	63.3	145	2	Q924R4_MOUSE	Q924r4 mus musculus
21	425	63.2	519	2	Q5BBM2_HUMAN	Q5ebm2 homo sapien
22	424.5	63.2	617	2	Q4KML5_MOUSE	Q4km15 mus musculus
23	422	62.8	147	2	Q925S3_MOUSE	Q925b3 mus musculus
24	420	62.5	157	2	Q95978_HUMAN	Q95978 homo sapien
25	419.5	62.4	475	2	Q8N095_HUMAN	Q8n095 homo sapien
26	418.5	62.4	470	2	Q7TMK1_MOUSE	Q7tmk1 mus musculus
27	418.5	62.3	118	1	Q8VY24_HUMAN	P06330 mus musculus
28	418	62.2	117	2	Q924R9_HUMAN	Q9qxe9 mus musculus
29	417	62.1	472	2	Q6uJA7_MOUSE	Q6pja7 mus musculus
30	417	62.0	473	2	Q9B8L4_MOUSE	Q99144 mus musculus
31	416.5	62.0	463	2	Q9BL4C_MOUSE	Q99145 mus musculus
RESULT 2						
Q9uL94_HUMAN						
PRELIMINARY;						
ID	Q9uL94_HUMAN	PRELIMINARY;				
AC	Q9uL94;					
DT	01-MAY-2000 (TREMBLrel. 13, Created)					
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)					
DB	Myosin-reactive immunoglobulin heavy chain variable region (Fragment).					
DE	Homo sapiens (Human)					
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bucardiidae; Gobiidae; Gobiomorphidae; Gobiomorphoidea; Gobiomorpha; Gobiomorphae; Gobiomorphae;					

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE,  
 RX MEDLINE:96277139; PubMed:9614934; DOI:10.1006/clin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin"-reactive autoantibodies in rheumatic carditis and normal  
 fetus.";  
 Clin. Immunol. Immunopathol. 87:184-192 (1998).  
 RL EMBL; AF035019; INQ;  
 DR HSSP; P01751; INQ;  
 DR Ensembl; ENSG0000130076; Homo sapiens.  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 119 AA; 13205 MW; 13864F5345F4A16B CRC64;  
 Query Match 73.5%; Score 494; DB 2; Length 119;  
 Best Local Similarity 76.0%; Pred. No. 2.8e-41;  
 Matches 95; Conservative 10; Mismatches 14; Indels 6; Gaps 1;  
 Qy 1 QVQLVQSGAVKPGASVKVSKASGIFTSDINWVQATGQGLEWMGWINPNSGNTDY 60  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 1 EVQLVQSGAVKPGASVKVSKASGIFTSDYMMWVQAPGQGLEWMGWINPNSGNTY 60  
 Qy 61 AQKFGQRTMTRDTISIATAYMELSSLRSDTAYCVRGFSYDDYYGMDWQGQTT 120  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 61 AQKFGQRTMTRDTISIATAYMELSSLRSDTAYCVRGFSYDDYYGMDWQGQTT 120  
 :|||||:|||||:|||||:|||||:|||||:  
 Qy 121 VTVSS 125  
 Db 115 VTVSS 119

RESULT 3  
 Q9UL95\_HUMAN  
 ID Q9UL95\_HUMAN PRELIMINARY;  
 AC DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DB Myosin-reactive immunoglobulin heavy chain variable region  
 OS Homo sapiens (Human).  
 Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Homo sapiens; Metazoa; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 Homo sapiens (Human).  
 OC Homo  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE,  
 RX MEDLINE:98277139; PubMed:9614934; DOI:10.1006/clin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin"-reactive autoantibodies in rheumatic carditis and normal  
 fetus.";  
 Clin. Immunol. Immunopathol. 87:184-192 (1998).  
 RL EMBL; AF035019; AF056255.1; -; mRNA.  
 DR HSSP; P01751; INQ;  
 DR Ensembl; ENSG0000130076; Homo sapiens.  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488ERC CRC64;  
 Query Match 73.5%; Score 494; DB 2; Length 125;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE,  
 RX MEDLINE:96277139; PubMed:9614934; DOI:10.1006/clin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin"-reactive autoantibodies in rheumatic carditis and normal  
 fetus.";  
 Clin. Immunol. Immunopathol. 87:184-192 (1998).  
 RL EMBL; AF035019; AF056255.1; -; mRNA.  
 DR HSSP; P01751; INQ;  
 DR Ensembl; ENSG0000130076; Homo sapiens.  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488ERC CRC64;  
 Query Match 73.5%; Score 494; DB 2; Length 125;

Best Local Similarity 76.0%; Pred. No. 3e-41;  
 Matches 95; Conservative 9; Mismatches 21; Indels 0; Gaps 0;  
 Qy 1 QVQLVQSGAVKPGASVKVSKASGIFTSDINWVQATGQGLEWMGWINPNSGNTDY 60  
 :|||||:  
 Db 1 EVQLVQSGAVKPGASVKVSKASGIFTSDYMMWVQAPGQGLEWMGWINPNSGNTY 60  
 Qy 61 AQKFGQRTMTRDTISIATAYMELSSLRSDTAYCVRGFSYDDYYGMDWQGQTT 120  
 :|||||:  
 Db 61 AQKFGQRTMTRDTISIATAYMELSSLRSDTAYCVRGFSYDDYYGMDWQGQTT 120  
 :|||||:  
 Qy 121 VTVSS 125  
 Db 121 VTVSS 125  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM00406; IgV; 2.  
 DR PROSITE; PS50835; Ig\_LIKE; 2.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 244 AA; 26127 MW; 4BF1786833892BF CRC64;  
 Query Match 73.1%; Score 491; DB 2; Length 244;  
 Best Local Similarity 75.4%; Pred. No. 1.3e-40;  
 Matches 95; Conservative 13; Mismatches 12; Indels 6; Gaps 2;  
 Qy 1 QVQLVQSGAVKPGASVKVSKASGIFTSDINWVQATGQGLEWMGWINPNSGNTDY 60  
 :|||||:  
 Db 1 EVQLVQSGAVKPGASVKVSKASGIFTSDYMMWVQAPGQGLEWMGWINPNSGNTDY 60  
 Qy 61 AQKFGQRTMTRDTISIATAYMELSSLRSDTAYCVRGFSYDDYYGMDWQGQTT 119  
 :|||||:  
 Db 61 AQKFGQRTMTRDTISIATAYMELSSLRSDTAYCVRGFSYDDYYGMDWQGQTT 119  
 :|||||:  
 Qy 120 VTVSS 125  
 Db 116 VTVSS 121

RESULT 5  
 HVIC\_HUMAN  
 ID HVIC\_HUMAN STANDARD;  
 AC P0174;  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488ERC CRC64;  
 Query Match 73.5%; Score 494; DB 2; Length 125;

Best Local Similarity 76.0%; Pred. No. 3e-41;  
 Matches 95; Conservative 9; Mismatches 21; Indels 0; Gaps 0;  
 Qy 1 QVQLVQSGAVKPGASVKVSKASGIFTSDINWVQATGQGLEWMGWINPNSGNTDY 60  
 :|||||:  
 Db 1 EVQLVQSGAVKPGASVKVSKASGIFTSDYMMWVQAPGQGLEWMGWINPNSGNTDY 60  
 Qy 61 AQKFGQRTMTRDTISIATAYMELSSLRSDTAYCVRGFSYDDYYGMDWQGQTT 120  
 :|||||:  
 Db 61 AQKFGQRTMTRDTISIATAYMELSSLRSDTAYCVRGFSYDDYYGMDWQGQTT 120  
 :|||||:  
 Qy 121 VTVSS 125  
 Db 121 VTVSS 125  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM00406; IgV; 2.  
 DR PROSITE; PS50835; Ig\_LIKE; 2.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 244 AA; 26127 MW; 4BF1786833892BF CRC64;  
 Query Match 73.1%; Score 491; DB 2; Length 244;  
 Best Local Similarity 75.4%; Pred. No. 1.3e-40;  
 Matches 95; Conservative 13; Mismatches 12; Indels 6; Gaps 2;  
 Qy 1 QVQLVQSGAVKPGASVKVSKASGIFTSDINWVQATGQGLEWMGWINPNSGNTDY 60  
 :|||||:  
 Db 1 EVQLVQSGAVKPGASVKVSKASGIFTSDYMMWVQAPGQGLEWMGWINPNSGNTDY 60  
 Qy 61 AQKFGQRTMTRDTISIATAYMELSSLRSDTAYCVRGFSYDDYYGMDWQGQTT 119  
 :|||||:  
 Db 61 AQKFGQRTMTRDTISIATAYMELSSLRSDTAYCVRGFSYDDYYGMDWQGQTT 119  
 :|||||:  
 Qy 120 VTVSS 125  
 Db 116 VTVSS 121

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBITaxonID=9606;  
RN [1] NUCLEOTIDE SEQUENCE;  
RX MEDLINE=8305234; PubMed=6816565;  
RA Kenten J.H., Moijaard H.V., Houghton M., Derbyshire R.B., Viney J.,  
Bell L.O., Gould H.J.;  
RN "Cloning and sequence determination of the gene for the human  
immunoglobulin epsilon chain expressed in a myeloma cell line.";  
RN [2] PROTEIN SEQUENCE OF 20-147;  
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;  
RL (In) Bach M.K. (eds.)  
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,  
Marcel Dekker, New York (1978).  
CC -1- MISCELLANEOUS: This epsilon chain was isolated from a myeloma  
protein.  
-1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
CC  
DR HSSP; P01751; INQB.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:003823; F:antigen binding; NAS.  
DR GO; GO:000955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR SMART; SM00406; Ig\_v.  
DR PROSITE; PS50835; Ig\_LIKE;  
DR KRW Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region; Pyrrolidone carboxylic acid; Signal.  
PT SIGNAL 1 19  
FT CHAIN 20 147 Ig heavy chain V-I region ND.  
FT DOMAIN 20 131 Ig-like.  
FT MOD\_RES 20 20 Pyrrolidone carboxylic acid.  
FT DISULFID 41 115 T -> V (in Ref. 2).  
FT CONFLICT 21 21 IH -> HI (in Ref. 2).  
FT CONFLICT 53 54 VG -> GV (in Ref. 2).  
FT CONFLICT 67 68 Missing (in Ref. 2).  
FT CONFLICT 125 125  
FT NON\_TER 147 147  
SQ SEQUENCE 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 48.5%; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-40; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

DR	Pfam; PF07654; C1-set; 2.	
DR	SMART; SM00409; Ig; 4.	
DR	SMART; SM00407; IgC1; 3.	
DR	SMART; SM00406; IgV; 1.	
DR	PROSITE; PS00230; Ig_MHC; UNKNOWN_2.	
KW	Hypothetical protein.	
FT	NON_TER 1	
SQ	SEQUENCE 498 AA; 54125 MW; 40B3208A84E03B46 CRC64;	
Query Match	Score 47.8%; DB 2; Length 498; Best Local Similarity 74.6%; Pred. No. 5e-39; Mismatches 11; Indels 3; Gaps 2;	
Matches	94; Conservative	
QY	1 QVQLYQGAVYKPGASVKVSKASGTYFTSDYTDINWROATGQCLEMWMGINPNSGNTDY 60 35 QVQLYQGADYKPGASVKVSKASGTYFTNPFINWROAQGPQGEMGINPRDGSTK 94	
Db	61 AQKFGQRVMTRDTSLTAYMELSSRLSEDTAIYVCCR-GFGSYNTYDGYMDWGGT 119 95 AQRFQGRVSMTRDTSTTIVMELSSRLSEDTAMFPCARAGPGYGTSAISYF-DYWGGT 152	
QY	120 TVTVSS 125	
Db	153 LTVVSS 158	
RESULT 8	Q8W724 HUMAN PRELIMINARY; PRT; 497 AA.	
AC	Q8W724_HUMAN PRELIMINARY; PRT; 497 AA.	
DR	01-MAR-2002 (TREMBLrel. 20, Created) 01-MAR-2002 (TREMBLrel. 20, Last sequence update) 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	
DR	SNC56 protein.	
DE	Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	
OC	Homo.	
OX	NCBI_TaxID:9606;	
RN	[1] NUCLEOTIDE SEQUENCE.	
RP	NUCLEOTIDE SEQUENCE.	
RA	Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.; Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.	
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF283666; AAL6987.1; - ; mRNA.	
DR	HSSP; P01876; 10W0.	
DR	SMR; Q8W724; 267-475.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003597; Ig_c1.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR00596; Ig_v.	
DR	Pfam; PF07654; C1-set; 2.	
DR	SMART; SM00406; IgV; 1.	
DR	PROSITE; PS00835; Ig_LIKE; 4.	
KW	Immunoglobulin domain.	
SEQUENCE	497 AA; 53666 MW; F24D08DFA5A663E5 CRC64;	
Query Match	Score 70.5%; DB 2; Length 497; Best Local Similarity 70.0%; Pred. No. 1.4e-18; Mismatches 13; Indels 10; Gaps 2;	
Matches	91; Conservative	
QY	1 QVQLYQGAVYKPGASVKVSKASGTYFTSDYTDINWROATGQCLEMWMGINPNSGNTDY 60 20 QEQLEQSGAVYTKPGASVKVSKASGTYFTSDYTDINWROATGQCLEMWMGINPNSGNTDY 79	
Db	61 AQKFGQRVMTRDTSLTAYMELSSRLSEDTAIYVCCR-GFGSYNTYDGYMDWGGT 115 80 AQKFGQRVLTFRDTSINTAYVNLSSLSTEDSAIYFARGNLRGGRGFTYW----FDPW 134	
QY	116 QGQTIVVSS 125 135 GHGTIVVSS 144	
Db	Query Match 70.0%; Score 470.5%; DB 2; Length 500; Best Local Similarity 71.9%; Pred. No. 3.1e-38; Mismatches 92; Conservative 11; Indels 3; Gaps 1 QVQLYQGAVYKPGASVKVSKASGTYFTSDYTDINWROATGQCLEMWMGINPNSGNTDY 60 20 QVHLVQSGAVYTKPGASVKVSKASGTYFTSDYTDINWROATGQCLEMWMGINPNSGNTDY 79	
QY	61 AQKFGQRVMTRDTSLTAYMELSSRLSEDTAIYVCCR-GFGSYNTYDGYMDWGGT 115 80 AKKFGQRVLTFRDTSINTAYVNLSSLSTEDSAIYFARGNLRGGRGFTYW----FDPW 134	
Db	QY	118 GTTVVSS 125





RESULT 15  
 Q6P089\_HUMAN PRELIMINARY; PRT; 480 AA.  
 AC Q6P089;  
 DR 05-JUL-2004 (TREMBLref. 27, Created)  
 DR 05-JUL-2004 (TREMBLref. 27, Last sequence update)  
 DR 05-JUL-2004 (TREMBLref. 27, Last annotation update)  
 DB Hypothetical Protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 Homo.  
 OM NCBI\_TAXID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Glandular pool- thyroid;  
 RX MEDLINE=22388257; PubMed=1247942; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Groner L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaido M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinchi P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalain D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnarch A., Schein J.B., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Glandular pool- thyroid;  
 RA Strausberg R.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC056733; AAH65733.1; - mRNA.  
 DR HSSP; P01751; 1A6W.  
 DR SMR; Q6P089; 250-458.  
 DR InterPro; IPR003599; Ig-1.  
 DR InterPro; IPR007110; Ig-1-like.  
 DR InterPro; IPR003597; Ig\_G1.  
 DR InterPro; IPR003106; Ig\_MRC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pf07554; Cl-set; 2.  
 DR SMART; SM00409; Ig; 4.  
 DR SMART; SM00407; IgC1; 3.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 4.  
 DR PROSITE; PS00290; Ig\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 480 AA; 51997 MW; 2E286C57E4F0ED65 CRC64;  
 Query Match 65.2%; Score 438; DB 2; Length 480;  
 Best Local Similarity 68.5%; Pred. No. 5; 2e-35; Mismatches 13; Indels 8; Gaps 2;  
 Matches 87; Conservative 13; Mismatches 19; Indels 8; Gaps 2;  
 Qy 1 QVQLVQSGAEVKKPGASVVKVSKASGYFTSDINWQATGQGLEWMGMINPNSGNTDY 60  
 |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 20 QYQLVQSGAEVKKPGASVVKVSKASGYFTSDINWQATGQGLEWMGMINPNSGNTDY 79  
 |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Qy 61 AOKPQGRVTVMTDTS1STAYMELISSLSESDTAIYCVRGFGF--YSNTYDYYGMDWQGQ 118  
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 80 AEKPGQGRVTVITDTS1NTAYMELTS1KSDDFALYYCARGHSDWSSRYFDY-----WGQG 133  
 Qy 119 TTVTVSS 125

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OM protein - protein search, using sw mode]

Run on: May 15, 2006, 16:53:57 ; Search time 126.077 Seconds

(without alignments)

376.380 Million cell updates/sec

Title: US-10-041-860-49

Perfect score: 558

Sequence: 1 EIVITQSPGTLSLSPGERAT.....CQQYGSPPCSFGQGTLEIK 108

Scoring table: BLOSUM62 Gapopen 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:

2443163

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21:\*

1: GeneseqP1980s:\*

2: GeneseqP1990s:\*

3: GeneseqP2000s:\*

4: GeneseqP2001s:\*

5: GeneseqP2002s:\*

6: GeneseqP2003s:\*

7: GeneseqP2003bs:\*

8: GeneseqP2004s:\*

9: GeneseqP2005s:\*

### RESULT 1

ADK18625

ID ADK18625 standard; protein; 108 AA.

XX ADK18625;

AC XX

DT DT 06-MAY-2004 (first entry)

XX DB Anti-human PDGF-D antibody light chain protein sequence.

XX KW antiinflammatory; immunomodulator; cytostatic; gene therapy.

XX OS Homo sapiens.

XX PN WO2003057857-A2.

XX PD 17-JUL-2003.

XX PP 06-JAN-2003; 2003WO-US0000398.

XX XX

XX PR 07-JAN-2003; 2002US-00041860.

XX XX

XX PA (ABGENIX INC.

XX PI Corvalan JRF, Jia X, Peng X, Yang X, Chen F, Gazit G, Weber R;

XX PI Bezabeh B;

XX DR WPI; 2003-587119/55.

XX XX

XX PT New human monoclonal antibody that binds to platelet-derived growth

PT factor-D (PDGF-D), useful for treating chronic and recurrent human

PT diseases, such as inflammation, autoimmunity and cancer.

PT Disclosure: SEQ ID NO 49; 255PP; English.

XX XX

XX PS

XX CC The invention relates to human monoclonal antibody that binds to

CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for

CC treating chronic and recurrent human diseases, such as inflammation,

CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are

CC useful for modulating collagen formation, and for staging various

CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were

CC generated using an active protein fragment of the gene product from the

CC clone 3066188.0.99 arising in the conditioned medium obtained when

CC HK293 cells are transfected with the plasmid pCEP4/Seq-3066188. This

CC sequence corresponds to a protein used in the invention.

XX XX

XX SQ Sequence 108 AA;

SQ

### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	558	100.0	108	7	ADK18625	Adk18625 Anti-human
2	558	100.0	108	7	ADK18951	Adk18951 Anti-human
3	558	100.0	108	7	ADK18835	Adk18835 Anti-human
4	558	100.0	108	7	ADK18801	Adk18801 Anti-human
5	558	100.0	108	8	ADU25394	Adl25394 Human mAb
6	535	95.9	108	9	ADY26769	Ady26769 Anti-NGF-
7	535	95.9	108	9	ADY26816	Ady26816 Human ant
8	535	95.9	128	9	ADZ57709	Adz57709 Germinaline
9	535	95.9	129	2	ABP38672	Vk325-Tk2
10	533	95.5	108	7	ADP0986	Adp0986 Murine-ex
11	533	95.5	130	6	ABJ36930	Anti-CD40
12	533	95.5	384	4	Aam24101	Human EST
13	532	95.3	108	8	ADQ14703	Modified
14	532	95.3	108	9	ADY44439	Adv44439 Pax116 va
15	532	95.3	108	9	ABE12911	Antibody
16	532	95.3	109	8	ADP46971	Murine li
17	532	95.3	112	9	ADY44477	Anti-teta
18	532	95.3	120	7	ADP40551	381/4G11
19	532	95.3	130	9	ABE12948	Antibody
20	532	95.3	215	8	ADQ16702	Modified
21	532	95.3	215	9	ADY44438	Adv44438 pAX116 va
22	532	95.3	215	9	ABE12910	Antibody
23	532	95.3	239	9	ADY44458	Adv44458 Anti-teta
24	532	95.3	239	9	ABE12929	Antibody



KW antiinflammatory; immunomodulator; cytostatic; gene therapy.

OS Homo sapiens.

XX WO2003057857-A2.

XX 17-JUL-2003.

XX 06-JAN-2003; 2003WO-US000398.

XX 07-JAN-2002; 2002US-00041860.

XX (AEGE-) ABGENIX INC.

PI Corvalan JRF, Jia X, Peng X, Yang X, Chen F, Gazit G, Weber R; Bezabeh B;

WPI; 2003-587119/55.

XX New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.

PT Disclosure: SEQ ID NO 225; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the HEK293 cells are transfected with the plasmid pCBP/Sec-30664188. This sequence corresponds to a protein used in the invention.

XX Sequence 108 AA;

PP 16-SEP-2003; 2003WO-US029414.

XX PR 16-SEP-2002; 2002US-0411137P.

XX (ABGB-) ABGENIX INC.

PA (CURA-) CURAGEN CORP.

XX PI Ploegh J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;

XX DR WPI; 2004-269881/25.

XX N-PSDB; ADU25393.

XX Use of an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD) for preparing a medicament for treating nephritis.

XX Disclosure: SEQ ID NO 4; 115pp; English.

PP The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described:

CC (1) a method of treating nephritis; (2) a method of preparing a medicament for treating nephritis; (3) a method of inhibiting mesangial cell proliferation; and (4) a method

CC of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antiinflammatory, dermatological, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a

CC medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mab) variable region sequence, which is used in the exemplification of the present invention.

XX Sequence 108 AA;

CC Query Match 100.0%; Score 558; DB 8; Length 108;

CC Best Local Similarity 100.0%; Pred. No. 4.1e-35;

CC Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 BIVLTQSPGTLSLSPGERATLSRASOSVSSYLLAQYQKPGQAPRILYATSSRATGIP 60

CC Db 1 BIVLTQSPGTLSLSPGERATLSRASOSVSSYLLAQYQKPGQAPRILYATSSRATGIP 60

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC Db 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

CC QY 61 DRFGSGSGSGTGTDTLTSRLPEDFAYVYQQYGSSPCSRGQGTQLEIK 108

&lt;p

PI Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F;  
 XX DR WPI; 2005-202606/21.

XX New human anti-nerve growth factor (NGF) neutralizing antibodies useful for manufacturing a medicament for treating painful disorders (e.g. acute pain) or conditions associated with increased expression or sensitivity to NGF.

XX Claim 33; SEQ ID NO 84; 190pp; English.

XX The invention describes an isolated human antibody that interacts with or binds specifically to human nerve growth factor (NGF) and neutralize the function of NGF. Also described are: methods of treating a condition caused by increased expression of NGF or increased sensitivity to NGF in a patient; methods for detecting NGF in a biological sample; an NGF specific binding agent comprising any of the 59 amino acid sequences comprising, for e.g., 123, 107 or 14 amino acids, as mentioned in the specification, and where the binding agent can bind to NGF; a pharmaceutical composition comprising a pharmaceutical carrier and a therapeutic amount of the antibody or binding agent cited above; or a medicament for treating a painful disorder or condition associated with increased expression of NGF or increased sensitivity to NGF, the medicament comprising a pharmaceutical amount of a monoclonal antibody or its immunologically functional immunoglobulin fragment, or pharmaceutical salts of the monoclonal antibody or the fragment, where the monoclonal antibody is at least one of the monoclonal antibody cited above, and a pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or polynucleotide that encodes the above antibody or binding agent; an isolated cell line that produces the above antibody or binding agent; an expression vector comprising the above polynucleotide; and a host cell comprising the nucleic acid or expression vector. The composition (including the antibody) and methods are useful for manufacturing a medicament for treating a painful disorder (e.g. acute pain, dental pain, or pain from trauma or cancer), or a condition associated with increased expression of NGF or increased sensitivity to NGF. This is the amino acid sequence of a human NGF antibody light chain variable region.

XX Sequence 108 AA;

Query Match 95.9%; Score 535; DB 9; Length 108;  
 Best Local Similarity 96.3%; Pred. No. 2.3e-33; Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0; SQ Sequence 108 AA;

Qy 1 EIVLQSPGTTLSLSPGERATLSCRASQSVSSESYLAWYQOKPGOAPRLIYATSSRATGIP 60  
 Db 1 EIVLQSPGTTLSLSPGERATLSCRASQSVSSESYLAWYQOKPGOAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSSGDTPLTISRLPEDFAVVYQQYGSSPCSFGGTKEIK 108  
 Db 61 DRFGSGSSGDTPLTISRLPEDFAVVYQQYGSSPCSFGGTKEIK 108

Qy 61 DRFGSGSSGDTPLTISRLPEDFAVVYQQYGSSPYFGGTKEIK 108  
 Db 61 DRFGSGSSGDTPLTISRLPEDFAVVYQQYGSSPYFGGTKEIK 108

RESULT 7  
 ADY26816 standard; protein; 108 AA.  
 ID ADY26816 standard; protein; 108 AA.  
 XX AC ADY26816;  
 XX DT 19-MAY-2005 (first entry)  
 XX DB Human anti-NGF-antibody light chain SEQ ID NO 131.  
 XX KW analgesic; gene therapy; antibody engineering; pharmaceutical; pain; neurological disease; NGF; nerve growth factor; light chain.  
 XX OS Homo sapiens.  
 XX PN WO2005019266-A2.  
 XX PD 03-MAR-2005.  
 XX PP 15-JUL-2004; 2004WO-US022876.

PR 15-JUL-2003; 2003US-0487431P.  
 XX PA (AMGEN INC.  
 XX PI Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F;  
 XX DR WPI; 2005-202606/21.

XX New human anti-nerve growth factor (NGF) neutralizing antibodies useful for manufacturing a medicament for treating painful disorders (e.g. acute pain) or conditions associated with increased expression or sensitivity to NGF.

XX PS Claim 33; SEQ ID NO 131; 190pp; English.

XX The invention describes an isolated human antibody that interacts with or binds specifically to human nerve growth factor (NGF) and neutralize the function of NGF. Also described are: methods of treating a condition caused by increased expression of NGF or increased sensitivity to NGF in a patient; methods for detecting NGF in a biological sample; an NGF specific binding agent comprising any of the 59 amino acid sequences comprising, for e.g., 123, 107 or 14 amino acids, as mentioned in the specification, and where the binding agent can bind to NGF; a pharmaceutical composition comprising a pharmaceutical carrier and a therapeutic amount of the antibody or binding agent cited above; or a medicament for treating a painful disorder or condition associated with increased expression of NGF or increased sensitivity to NGF, the medicament comprising a pharmaceutical amount of a monoclonal antibody or its immunologically functional immunoglobulin fragment, or pharmaceutical salts of the monoclonal antibody or the fragment, where the monoclonal antibody is at least one of the monoclonal antibody cited above, and a pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or polynucleotide that encodes the above antibody or binding agent; an isolated cell line that produces the above antibody or binding agent; an expression vector comprising the above polynucleotide; and a host cell comprising the nucleic acid or expression vector. The composition (including the antibody) and methods are useful for manufacturing a medicament for treating a painful disorder (e.g. acute pain, dental pain, or pain from trauma or cancer), or a condition associated with increased expression of NGF or increased sensitivity to NGF. This is the amino acid sequence of a human NGF antibody light chain.

Query Match 95.9%; Score 535; DB 9; Length 108;  
 Best Local Similarity 96.3%; Pred. No. 2.3e-33; Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLQSPGTTLSLSPGERATLSCRASQSVSSESYLAWYQOKPGOAPRLIYATSSRATGIP 60  
 Db 1 EIVLQSPGTTLSLSPGERATLSCRASQSVSSESYLAWYQOKPGOAPRLIYATSSRATGIP 60

Qy 1 EIVLQSPGTTLSLSPGERATLSCRASQSVSSESYLAWYQOKPGOAPRLIYATSSRATGIP 60  
 Db 1 EIVLQSPGTTLSLSPGERATLSCRASQSVSSESYLAWYQOKPGOAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSSGDTPLTISRLPEDFAVVYQQYGSSPCSFGGTKEIK 108  
 Db 61 DRFGSGSSGDTPLTISRLPEDFAVVYQQYGSSPCSFGGTKEIK 108

Qy 61 DRFGSGSSGDTPLTISRLPEDFAVVYQQYGSSPYFGGTKEIK 108  
 Db 61 DRFGSGSSGDTPLTISRLPEDFAVVYQQYGSSPYFGGTKEIK 108

RESULT 8  
 ADZ57709  
 ID ADZ57709 standard; protein; 128 AA.  
 XX AC ADZ57709;  
 XX DT 30-JUN-2005 (first entry)  
 XX DB Germline antibody A27VKA.Jk2 light chain protein.

XX KW antibody engineering; cytosstatic; vulnerability; vasoconstrictor; cardiotonic; monoclonal antibody; heavy chain; light chain; wound healing; skin ulcer; KW Gastric/oesophageal ulcer; ischaemia; transplant rejection; myocardial infarction; reperfusion injury; restenosis; angioplasty; vascular disease; cancer; retinopathy; endometriosis;

Sequence 128 AA:						
SQ	Query	Match	Score	DB	Length	
	Qy	Query Match	95.9%	Score 535;	DB 9;	Length 128;
	Qy	Best Local Similarity	96.3%	Pred. No. 2.7e-33;		
	Qy	Matches 104;	Conservative	1; Mismatches	3;	Indels 0;
	Qy					Gaps 0;
	Ddb					
	Qy	1 BIVLTQSPGTULS	95.9%	Score 535;	DB 9;	Length 128;
	Qy	SUPERATLSCRAQS	95.9%	Pred. No. 2.7e-33;		
	Qy	QVSSSYLWYQQK	95.9%	1; Mismatches	3;	Indels 0;
	Qy	QAPRLLIYATSSRATGIP	95.9%			Gaps 0;
	Qy	61 DRPSGSQSGTDTFLTIS	95.9%			
	Qy	RLPDTATYCCQYGGSPCSFGOTKLTK	95.9%			
	Qy	108	95.9%			

similarity. By nucleotide sequence analysis, F105 appears to be derived from a member of the Vκ III subgroup gene family. (Updated on 25-MAR-2003 to correct PN field.)



Qy 61 DRPGSGSGCTDFLTISRLPEDFAVYCCQXGSSPCSFQGQTKLEIK 108  
 Db 81 DRPGSGSGCTDFLTISRLPEDFAVYCCQXGSSPCSFQGQTKLEIK 128

RESULT 1.2  
 AAM24101  
 ID AAM24101 standard; protein; 384 AA.  
 XX  
 AC AAM24101;  
 XX  
 DT 12-OCT-2001 (first entry)  
 XX  
 DE Human EST encoded protein SEQ ID NO: 1626.  
 XX  
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;  
 KW gene therapy; nutrition.  
 OS Homo sapiens.  
 XX  
 PN WO200154477-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PP 25-JAN-2001; 2001WO-US002687.  
 XX  
 PR 25-JAN-2000; 2000US-00491404.  
 PR 17-JUL-2000; 2000US-00617746.  
 PR 03-AUG-2000; 2000US-00631451.  
 PR 15-SEP-2000; 2000US-006638870.  
 XX  
 PA (HYSEQ INC.).

XX  
 PI Tang XT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
 XX  
 DR WBI; 2001-476164/51.  
 DR N-PSDB; AAH38760

XX  
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
 antibodies and research use.  
 PS Claim 20; Page 1102-1103; 1275pp; English.

XX  
 CC The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a  
 CC protein of the invention.  
 XX  
 SQ Sequence 384 AA;

Query Match 95.5%; Score 533; DB 4; Length 384;  
 Best Local Similarity 95.4%; Pred. No. 1e-34;  
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSEYLAWQKQGQAPRLIVATSSRATGIP 60  
 Db 167 EIVLTQSPGTLSLSPGERATLSCRASQVSSEYLAWQKQGQAPRLIVGASSRATGIP 226

Qy 61 DRFGSGSGGTDFLTISRLPEDFAVYCCQYGSPPCSFGQGTCLEIK 108  
 Db 227 DRFGSGSGGTDFLTISRLPEDFAVYCCQYGSPPCSFGQGTCLEIK 274

RESULT 1.4  
 ADV4439  
 ID ADV4439 standard; protein; 108 AA.  
 XX  
 AC ADV4439;  
 XX  
 DT 10-MAR-2005 (first entry)  
 XX  
 DB PAX116 variable light chain variable region.

XX  
 KW anti-HIV; cytostatic; gene therapy; antibody engineering; diagnosis;  
 KW HIV-infection; anti-HIV; chemotherapy; bone marrow transplantation;  
 KW transplant rejection; prophylaxis; myeloproliferative disorder;

RESULT 1.3  
 ADQ16703  
 ID ADQ16703 standard; protein; 108 AA.

KW hematological disease; pax116.  
 XX KW Antibody; phage display; protein therapy; antibody engineering;  
 XX hemopoiesis; immunotherapy; Cardiant; Anti-diabetic; Anorectic; TPO;  
 KW cardiac failure; diabetes; obesity; light chain; tetanus toxoid; TPO;  
 KW thrombopoietin.  
 XX  
 PN WO2004108078-A2.  
 XX  
 XX 16-DEC-2004.  
 PD XX  
 XX PF 26-MAY-2004; 2004WO-US016574.  
 XX PR 02-JUN-2003; 2003US-00452590.  
 XX  
 PA (ALEX- ) ALEXION PHARM INC.  
 XX  
 PI Bowdish KS, Frederickson S, Renshaw M, Orenicia C;  
 XX DR 2005-031588/03.  
 XX  
 DR 2005-031588/03.  
 XX  
 PT New immunoglobulin molecule comprising a region where amino acid residues  
 PT corresponding to a portion of complementarity determining region (CDR) is  
 PT replaced with a peptide mimetic, useful for treating, e.g. HIV-infected  
 PT patients.  
 XX  
 PS Example 8; SEQ ID NO 123; 139pp; English.  
 XX  
 CC The invention describes an immunoglobulin molecule or its fragment  
 CC comprising: a region where amino acid residues corresponding to at least  
 CC a portion of two CDRs are replaced with a peptide mimetic selected from  
 CC an EPO mimetic or TPO mimetic; or a region where amino acid residues  
 CC corresponding to at least a portion of a CDR is replaced by a peptide  
 CC mimetic including SEQ ID NO. 126 (not defined in the specification),  
 CC where X at each occurrence represents any amino acid. Also described are:  
 CC a nucleic acid encoding an immunoglobulin molecule or its fragment; an  
 CC expression vector comprising the nucleic acid of (1); a host cell  
 CC transformed with the expression vector of (2); producing an  
 CC immunoglobulin molecule or its fragment; and a composition comprising the  
 CC immunoglobulin or its fragment and a pharmaceutical carrier. Also  
 CC disclosed are: engineering immunoglobulin molecules or fragments;  
 CC creation of a library of monoclonal antibodies; stimulating  
 CC proliferation, differentiation, or growth of megakaryocytes; and  
 CC activating a homodimeric receptor protein. The immunoglobulin molecules  
 CC are useful for treating HIV-infected patients, patients undergoing  
 CC chemotherapy, bone marrow transplant patients, stem cell transplant  
 CC patients, or patients suffering from myeloproliferative disorders. This  
 CC is the amino acid sequence of modified anti-tetanus toxoid antibody  
 CC pAX116 light chain variable region. The heavy chain of pAX116 comprises  
 CC two agonist TPO-mimetic peptides.  
 XX  
 SQ Sequence 108 AA;  
 Query Match 95.3%; Score 532; DB 9; Length 108;  
 Best Local Similarity 95.4%; Pred. No. 3.9e-33; Mismatches 2; Indels 0; Gaps 0;  
 Matches 103; Conservative 2;  
 Matches 103; Conservatve 2;  
 Qy 1 EIVLTQSPGTLSLSPGERATLSCRASVSSSYLAVYQKREGQAPLLVATSSATGIP 60  
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASVSSSYLAVYQKREGQAPLLVATSSATGIP 60  
 Qy 61 DRFGSGSGTDPFLTISRLPEDFAVVYCOQYGSPPCSFGQSTKLRKIK 108  
 Db 61 DRFGSGSGTDPFLTISRLPEDFAVVYCOQYGSPPCSFGQSTKLRKIK 108  
 RESULT 15  
 AEB12911 ID AEB12911 standard; protein; 108 AA.  
 XX  
 AC AEB12911;  
 XX  
 DT 08-SEP-2005 (first entry)  
 CC Antibody pAX116 light chain variable region.

CC tetanus toxoid Fab antibody with grafted TPO mimetic peptides in place  
CC of one or more of its CDRs.  
XX

SQ Sequence 108 AA;

Query Match 95.3%; Score 532; DB 9; Length 108;  
Best Local Similarity 95.4%; Pred. No. 3.9e-33;  
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 EIVLTQSPETLSLSPGERATLSRASQVSSSTLAWYQKPGQAPRLIYASSRATGIP 60  
Db 1 EIVLTQSPETLSLSPGERATLSRASQVSSSTLAWYQKPGQAPRLIYASSRATGIP 60  
Qy 61 DRFGSGSGSTDFTLTISLEPEDFAVYTCQQYQSSSPCSFGQGTRK 108  
Db 61 DRFGSGSGSTDFTLTISLEPEDFAVYTCQQYQSSSPWTFQGQTKVETK 108

Search completed: May 15, 2006, 16:58:53

Job time : 128.077 secs

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OM protein - protein search, using sw model

Run on: May 15, 2006, 17:04:12 ; Search time 30.5923 seconds

(without alignments)  
 291.870 Million cell updates/sec

Title: US-10-041-860-49

Perfect score: 558

Sequence: 1 BIVLQSPGTLSLSPGERAT.....CQQYGSSPCSFGQCTKLEIK 108

Scoring table: BLOSUM62

Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:

572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued Patents AA:  
 1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:/\*  
 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:/\*  
 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:/\*  
 4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:/\*  
 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:/\*  
 6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	530	95.0	108	1 US-08-232-081B-42	Sequence 42, App1
2	529	94.8	109	2 US-09-028-769B-16	Sequence 16, App1
3	529	94.8	109	2 US-09-490-070A-16	Sequence 16, App1
4	529	94.8	109	2 US-09-490-153-16	Sequence 16, App1
5	529	94.8	109	2 US-09-490-324-16	Sequence 16, App1
6	525	94.1	108	1 US-08-488-113B-150	Sequence 150, App1
7	525	94.1	108	1 US-08-647-484B-150	Sequence 150, App1
8	525	94.1	108	1 US-08-647-360-150	Sequence 150, App1
9	525	94.1	108	2 US-08-833-765-150	Sequence 150, App1
10	525	94.1	108	2 US-09-136-389-150	Sequence 150, App1
11	525	94.1	108	2 US-09-61-838-150	Sequence 150, App1
12	524	94.1	108	2 US-09-711-485-150	Sequence 150, App1
13	524	94.0	226	2 US-09-456-090A-50	Sequence 50, App1
14	524.5	94.0	226	2 US-09-456-090A-86	Sequence 86, App1
15	524.5	94.0	226	2 US-09-453-234-50	Sequence 50, App1
16	524.5	94.0	226	2 US-09-453-234-86	Sequence 86, App1
17	521	93.4	235	2 US-09-47-087-14	Sequence 14, App1
18	518	93.4	235	2 US-09-47-087-65	Sequence 65, App1
19	518.5	92.9	226	2 US-09-456-090A-80	Sequence 80, App1
20	518.5	92.9	226	2 US-09-456-234-80	Sequence 80, App1
21	518.5	92.8	236	2 US-09-853-34	Sequence 34, App1
22	518	92.8	108	2 US-09-245-274-178	Sequence 178, App1
23	518	92.8	108	2 US-09-84-798-178	Sequence 178, App1
24	512.5	92.0	236	2 US-09-853-38	Sequence 38, App1
25	512.5	91.8	226	2 US-09-456-090A-74	Sequence 74, App1
26	512.5	91.8	226	2 US-09-456-234-74	Sequence 74, App1
27	511.5	91.7	226	2 US-09-456-090A-42	Sequence 42, App1

#### ALIGNMENTS

RESULT 1  
 US-08-232-081B-42  
 ; Patent No. 5886152  
 / GENERAL INFORMATION:  
 / APPLICANT: NAKATANI, TOMOYUKI  
 / APPLICANT: GOMI, HIDENYUKI  
 / APPLICANT: WIDENES, JOHN  
 / APPLICANT: NOGUCHI, HIROSHI  
 / TITLE OF INVENTION: HUMANIZED B-B10  
 / NUMBER OF SEQUENCES: 42  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
 / STREET: PO BOX 747  
 / CITY: FALLS CHURCH  
 / STATE: VA  
 / COUNTRY: USA  
 / ZIP: 222040-0747  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patent In Release #1.0, Version #1.30  
 / CURRENT APPLICATION DATA:  
 / COMPUTER APPLICATION NUMBER: US/08/232, 081B  
 / FILING DATE:  
 / CLASSIFICATION: 424  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: SVENSSON, LEONARD R  
 / REGISTRATION NUMBER: 30, 330  
 / REFERENCE/DOCKET NUMBER: 20-3484  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (703) 205-8000  
 / TELEFAX: (703) 205-8050  
 / INFORMATION FOR SEQ ID NO: 42:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 108 amino acids  
 / TYPE: amino acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: peptide  
 / US-08-232-081B-42

Qy 61 DRFGSGSGTDTFLTISRLPEDPAVYCCQYGSPPSGQGQTKLBIK 108  
 Db 61 DRFGSGSGTDTFLTISRLPEDPAVYCCQYGSPPSGQGQTKLBIK 108

RESULT 2  
 US-09-025-769B-16  
 Sequence 16, Application US/09025769B  
 Patent No. 6300064  
 GENERAL INFORMATION:  
 APPLICANT: Knappik, Achim  
 APPLICANT: Pack, Peter  
 APPLICANT: Ilag, Vic  
 APPLICANT: Ge, Liming  
 APPLICANT: Moroney, Simon  
 APPLICANT: Plueckthun, Andreas  
 TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CURRENT APPLICATION DATA:  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10021

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/025,769B  
 FILING DATE: 18-FEB-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: James P. Haley, Jr., Esq.  
 REGISTRATION NUMBER: 27,794  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 596-9000  
 TELEFAX: (212) 596-9090  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 109 amino acids  
 TYPE: amino acid  
 STRANDBEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

RESULT 3  
 US-09-025-769B-16  
 Sequence 16, Application US/09025769B  
 Patent No. 6300064  
 GENERAL INFORMATION:  
 APPLICANT: Knappik, Achim  
 APPLICANT: Pack, Peter

Qy 61 DRFGSGSGTDTFLTISRLPEDPAVYCCQYGSPPSGQGQTKLBIK 108  
 Db 61 DRFGSGSGTDTFLTISRLPEDPAVYCCQYGSPPSGQGQTKLBIK 108

Query Match 94.8%; Score 529; DB 2; Length 109;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-42;  
 Matches 102; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 4  
 US-09-490-153-16

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSELYAQKRGQAPLLIYATSSRATGIP 60  
 Db 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSELYAQKRGQAPLLIYGASSRATGIP 60

Query Match 94.8%; Score 529; DB 2; Length 109;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-42;  
 Matches 102; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 5  
 US-09-490-070A-16

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSELYAQKRGQAPLLIYATSSRATGIP 60  
 Db 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSELYAQKRGQAPLLIYGASSRATGIP 60

Query Match 94.8%; Score 529; DB 2; Length 109;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-42;  
 Matches 102; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
 US-09-490-070A-16

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSELYAQKRGQAPLLIYATSSRATGIP 60  
 Db 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSELYAQKRGQAPLLIYGASSRATGIP 60

Query Match 94.8%; Score 529; DB 2; Length 109;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-42;  
 Matches 102; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 7  
 US-09-490-070A-16

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSELYAQKRGQAPLLIYATSSRATGIP 60  
 Db 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSELYAQKRGQAPLLIYGASSRATGIP 60

Query Match 94.8%; Score 529; DB 2; Length 109;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-42;  
 Matches 102; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 8  
 US-09-490-070A-16

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSELYAQKRGQAPLLIYATSSRATGIP 60  
 Db 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSELYAQKRGQAPLLIYGASSRATGIP 60

Query Match 94.8%; Score 529; DB 2; Length 109;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-42;  
 Matches 102; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 9  
 US-09-490-070A-16

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSELYAQKRGQAPLLIYATSSRATGIP 60  
 Db 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSELYAQKRGQAPLLIYGASSRATGIP 60

Query Match 94.8%; Score 529; DB 2; Length 109;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-42;  
 Matches 102; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 10  
 US-09-490-070A-16

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSELYAQKRGQAPLLIYATSSRATGIP 60  
 Db 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSELYAQKRGQAPLLIYGASSRATGIP 60

Query Match 94.8%; Score 529; DB 2; Length 109;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-42;  
 Matches 102; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 11  
 US-09-025-769B-16  
 Sequence 16, Application US/09025769B  
 Patent No. 6300064  
 GENERAL INFORMATION:  
 APPLICANT: Knappik, Achim  
 APPLICANT: Pack, Peter  
 APPLICANT: Ilag, Vic  
 APPLICANT: Ge, Liming  
 APPLICANT: Moroney, Simon  
 APPLICANT: Plueckthun, Andreas  
 TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CURRENT APPLICATION DATA:  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/025,769B  
 FILING DATE: 18-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Colin G. Sandercock, Esq.  
 REGISTRATION NUMBER: 31,398  
 REFERENCE/DOCKET NUMBER: 37629-00055  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 912-2000  
 TELEFAX: (202) 912-2020  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 109 amino acids  
 TYPE: amino acid  
 STRANDBEDNESS: <unknown>  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
 US-09-490-070A-16  
 Query Match 94.8%; Score 529; DB 2; Length 109;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-42;  
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 RESULT 12  
 US-09-490-153-16  
 Sequence 16, Application US/09490153  
 Patent No. 6706484  
 GENERAL INFORMATION:  
 APPLICANT: Knappik, Achim  
 APPLICANT: Pack, Peter  
 APPLICANT: Ilag, Vic  
 APPLICANT: Ge, Liming  
 APPLICANT: Moroney, Simon  
 APPLICANT: Plueckthun, Andreas  
 TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CURRENT APPLICATION DATA:  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/025,769B  
 FILING DATE: 18-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Colin G. Sandercock, Esq.  
 REGISTRATION NUMBER: 31,398  
 REFERENCE/DOCKET NUMBER: 37629-00055  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 912-2000  
 TELEFAX: (202) 912-2020  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 109 amino acids  
 TYPE: amino acid  
 STRANDBEDNESS: <unknown>  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
 US-09-490-153-16  
 Query Match 94.8%; Score 529; DB 2; Length 109;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-42;  
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

COUNTRY: USA  
 ZIP: 10021  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/490,153  
 FILING DATE: 24-Jan-2000  
 PRIORITY APPLICATION NUMBER: US/09/025,769B  
 FILING DATE: 18-FEB-1998  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: James F. Haley, Jr., Esq.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: MORPHO/5  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)596-9000  
 TELEFAX: (212)596-9090  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 109 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: <Unknown>  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: MORPHO/5  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)596-9000  
 TELEFAX: (212)596-9090  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 109 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: <Unknown>  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
 US-09-490-153-16

Query Match 94.8%; Score 529; DB 2; Length 109;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-42;  
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

RESULT 6  
 US-08-488-113B-150  
 ; Sequence 150, Application US/08488113B  
 ; Patent No. 5744580

GENERAL INFORMATION:  
 APPLICANT: Bacter, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Strodnika, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 Proteins  
 NUMBER OF SEQUENCES: 1659  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEER: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/488,113B  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/425,336  
 FILING DATE: 18-APR-1995  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,130  
 FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/187,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 150:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 108 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-488-113B-150

Query Match 94.1%; Score 525; DB 1; Length 108;  
 Best Local Similarity 94.4%; Pred. No. 4.3e-42;  
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASOSVSSYLVQKPGQAPRLIYATSSRATGIP 60  
 Db 1 BIVLTQSPGTLSLSPGERATLSCRASOSVSSYLVQKPGQAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSGTDFLTLSRLEPEDFAYYCOQYGSPPCSFGQGTKLKIK 108  
 Db 61 DRFGSGSGTDFLTLSRLEPEDFAYYCOQYGSPPCSFGQGTKLKIK 108

Qy 61 DRFGSGSGTDFLTLSRLEPEDFAYYCOQYGSPPXTFGQGTKLKIK 108  
 Db 61 DRFGSGSGTDFLTLSRLEPEDFAYYCOQYGSPPXTFGQGTKLKIK 108

RESULT 7  
 US-08-477-484B-150  
 Sequence 150, Application US/08477484B  
 Patent No. 5716699  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen P.  
 APPLICANT: Studnica, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 TITLE OF INVENTION: Proteins  
 NUMBER OF SEQUENCES: 169  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/477,484B  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/425,336  
 FILING DATE: 18-APR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/477,484B  
 FILING DATE: 12-MAY-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992

RESULT 8  
 US-08-646-360-150  
 Sequence 150, Application US/08646360  
 Patent No. 5837491  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen P.  
 APPLICANT: Studnica, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 TITLE OF INVENTION: Proteins  
 NUMBER OF SEQUENCES: 173  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/646,360  
 FILING DATE: 13-MAY-1996  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/05348  
 FILING DATE: 12-MAY-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/646,360  
 FILING DATE: 13-MAY-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE DOCKET NUMBER: 11022US09/200-70.P3.C3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 150:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 108 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-646-360-150

Query Match 94.1%; Score 525; DB 1; Length 108;  
 Best Local Similarity 94.4%; Pred. No. 4.3e-12; Indels 0; Gaps 0;  
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EIVLTQSGTTLSPGERATLSCASQVSSSYLAVYQKPGQAPRLIYATSSRATGIP 60  
 Db 1 EIVLTQSGTTLSPGERATLSCASQVSSSYLAVYQKPGQAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSGTDFLTISRLSLEPFDAYYCQOYGSPPCSFGQCTKLEIK 108  
 Db 61 DRFGSGSGTDFLTISRLSLEPFDAYYCQOYGSPPCSFGQCTKLEIK 108

RESULT 9  
 US-08-839-765-150  
 Sequence 150, Application US/08839765  
 Patent No. 6146631  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Studnica, Gary M.  
 APPLICANT: Studnica, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 TITLE OF INVENTION: Proteins  
 NUMBER OF SEQUENCES: 169  
 CURRENT APPLICATION DATA:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/839,765  
 FILING DATE: 15-APR-1997  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/425,336  
 FILING DATE: 18-APR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567

RESULT 10  
 US-09-136-389-150  
 Sequence 150, Application US/09136389  
 Patent No. 6146850  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Studnica, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 TITLE OF INVENTION: Proteins  
 NUMBER OF SEQUENCES: 173  
 CURRENT APPLICATION DATA:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/136,389  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/646,360  
 FILING DATE: 13-MAY-1996  
 APPLICATION NUMBER: PCT/US94/05348  
 FILING DATE: 12-MAY-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8869  
 TELEFAX: 650 388-1248  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 108 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-136-389-150

Query Match Similarity 94.1%; Score 525; DB 2; Length 108;  
 Best Local Similarity 94.4%; Pred. No. 4.3e-42; Indels 0; Gaps 0;  
 Matches 102; Conservative 2; Mismatches 4; DB 61

Query 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYATSSRATGIP 60  
 Db 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYASSRATGIP 60

Query 61 DRFGSGSGGTDDTTLTSRLBEPDFAVYYCQYGGSPCSFGGTTKLEIK 108  
 Db 61 DRFGSGSGGTDDTTLTSRLBEPDFAVYYCQYGGSPXTFGQGTTKVBK 108

RESULT 11  
 US-09-610-838-150  
 Sequence 150, Application US/09610838  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Studnitska, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 NUMBER OF SEQUENCES: 173  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/610,838  
 FILING DATE: 06-JUL-2000  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/136,389  
 FILING DATE: 18-AUG-1998  
 APPLICATION NUMBER: 08/646,360  
 FILING DATE: 13-MAY-1996  
 APPLICATION NUMBER: PCT/US94/05348  
 FILING DATE: 12-MAY-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707

APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 200-70-P4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEFAX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 150:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 108 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-610-838-150

Query Match Similarity 94.1%; Score 525; DB 2; Length 108;  
 Best Local Similarity 94.4%; Pred. No. 4.3e-42; Indels 0; Gaps 0;  
 Matches 102; Conservative 2; Mismatches 4; DB 61

Query 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYATSSRATGIP 60  
 Db 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYASSRATGIP 60

Query 61 DRFGSGSGGTDDTTLTSRLBEPDFAVYYCQYGGSPCSFGGTTKLEIK 108  
 Db 61 DRFGSGSGGTDDTTLTSRLBEPDFAVYYCQYGGSPXTFGQGTTKVBK 108

RESULT 12  
 US-09-711-485-150  
 Sequence 150, Application US/09711485  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Studnitska, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 NUMBER OF SEQUENCES: 165  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/711,485  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/839,765  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA: US 07/187,567  
 FILING DATE: 04-NOV-1991.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32, 918  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 150:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 108 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-711-485-150

Query Match 94.1%; Score 525; DB 2; Length 108;  
 Best Local Similarity 94.4%; Pred. No. 4.3e-42; Indels 0; Gaps 0;  
 Matches 102; Conservative 2; Mismatches 4; Delmiss 1; Gaps 1;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSSYLAQKPCQAPRLIYATSSRATGIP 60  
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSSYLAQKPCQAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSGTDFLTLSRLEPEDFAYVYCOQYCOQGSSPPYTFQGTRKLEIK 108  
 Db 61 DRFGSGSGTDFLTLSRLEPEDFAYVYCOQYCOQGSSPPYTFQGTRKLEIK 108

RESULT 15  
 US-09-453-234-50

Sequence 50, Application US/09453234  
 Patent No. 6794132

GENERAL INFORMATION:  
 APPLICANT: Buechler, Joe  
 APPLICANT: Valkirs, Gunars  
 APPLICANT: Gray, Jeff  
 APPLICANT: Lonberg, Nils  
 TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS  
 FILE REFERENCE: 020015-000200US  
 CURRENT APPLICATION NUMBER: US/09/456,090A  
 NUMBER OF SEQ ID NOS: 110  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 50  
 LENGTH: 226  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 OTHER INFORMATION: M1-23L  
 US-09-456-090A-50

Query Match 94.0%; Score 524.5; DB 2; Length 226;  
 Best Local Similarity 95.4%; Pred. No. 1.1e-41; Indels 1; Gaps 1;  
 Matches 104; Conservative 1; Mismatches 3; Delmiss 1; Gaps 1;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSSYLAQKPCQAPRLIYATSSRATGIP 60  
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSSYLAQKPCQAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSGTDFLTLSRLEPEDFAYVYCOQYCOQGSS-PCSPFGQGTKLEIK 108  
 Db 61 DRFGSGSGTDFLTLSRLEPEDFAYVYCOQYCOQGSSPPYTFQGTRKLEIK 108

RESULT 14  
 US-09-456-090A-86  
 Sequence 86, Application US/09456090A  
 Patent No. 6680209

Search completed: May 15, 2006, 17:06:01  
 Job time : 31.5923 secs

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Om protein - Protein search, using sw model

Run on: May 15, 2006, 17:19:47 ; Search time 108.927 Seconds (without alignments)

414.273 Million cell updates/sec

Title: US-10-041-860-49

Perfect score: 558

Sequence: 1 EIVITQSPGTLSIISPGERAT.....CQOYGSFCFSFGQGTLEIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA\_Main:  
1: /cgn2\_6/\_ptodata/1/\_pubpaas/US07\_PUBCOMB.pep:  
2: /cgn2\_6/\_ptodata/1/\_pubpaas/US08\_PUBCOMB.pep:  
3: /cgn2\_6/\_ptodata/1/\_pubpaas/US09\_PUBCOMB.pep:  
4: /cgn2\_6/\_ptodata/1/\_pubpaas/US10A\_PUBCOMB.pep:  
5: /cgn2\_6/\_ptodata/1/\_pubpaas/US10B\_PUBCOMB.pep:  
6: /cgn2\_6/\_ptodata/1/\_pubpaas/US11\_PUBCOMB.pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	558	100.0	108	4	US-10-041-860-49	Sequence 49, App
2	558	100.0	108	4	US-10-041-860-225	Sequence 225, App
3	558	100.0	108	4	US-10-041-860-259	Sequence 259, App
4	558	100.0	108	4	US-10-041-860-375	Sequence 375, App
5	558	100.0	108	4	US-10-065-383-4	Sequence 4, App
6	535	95.9	108	5	US-10-891-658-84	Sequence 84, App
7	535	95.9	108	5	US-10-891-658-131	Sequence 131, App
8	533	95.5	128	5	US-10-910-901-18	Sequence 18, App
9	533	95.5	108	4	US-10-109-762-156	Sequence 156, App
10	533	95.5	130	4	US-11-693-629-46	Sequence 46, App
11	532	95.3	108	4	US-10-307-724-123	Sequence 123, App
12	532	95.3	108	5	US-10-737-290-123	Sequence 123, App
13	532	95.3	109	5	US-11-275-962-27	Sequence 27, App
14	532	95.3	120	5	US-10-506-743-2	Sequence 2, App
15	532	95.3	130	5	US-10-737-290-161	Sequence 161, App
16	532	95.3	215	4	US-10-307-724-122	Sequence 122, App
17	532	95.3	215	5	US-10-737-290-122	Sequence 122, App
18	532	95.3	239	5	US-10-737-290-142	Sequence 142, App
19	530	95.0	384	4	US-10-291-265-804	Sequence 804, App
20	530	95.0	384	4	US-10-291-265-805	Sequence 805, App
21	530	95.0	384	4	US-10-291-265-806	Sequence 806, App
22	530	95.0	384	4	US-10-291-265-807	Sequence 807, App
23	529	94.8	108	4	US-10-269-711-21	Sequence 21, App
24	529	94.8	108	4	US-10-384-109-21	Sequence 21, App
25	528	94.6	108	3	US-09-948-109-21	Sequence 9, App
26	528	94.6	108	6	US-11-040-844-9	Sequence 9, App
27	526	94.3	108	4	US-10-338-366-4	Sequence 4, App

## ALIGNMENTS

RESULT 1  
US-10-041-860-49  
; Sequence 49, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gadi  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezaheb, Binyamin  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: AGENIX\_051A  
; CURRENT APPLICATION NUMBER: US/10/041,860  
; CURRENT FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 49  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-041-860-49

Query Match 108: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Best Local Similarity 100.0%; Score 550; DB 4; Length 108;  
Matches 108; Conservatice 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLQSPGTLSIISPGERATLSRASQSVSSYIILWYQQXPQGAQRLIVATSSRATGIP 60  
Db 1 EIVLQSPGTLSIISPGERATLSRASQSVSSYIILWYQQXPQGAQRLIVATSSRATGIP 60

Qy 61 DRFSSGSGSGTDFTLTSLSPEDFVAVYCCQYGSSPCSFSGGTKEIK 108  
Db 61 DRFSSGSGSGTDFTLTSLSPEDFVAVYCCQYGSSPCSFSGGTKEIK 108

RESULT 2  
US-10-041-860-225  
; Sequence 225, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gadi

APPLICANT: Weber, Richard  
 APPLICANT: Bezabeh, Binyam  
 TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES  
 TITLE OF INVENTION: THEREOF  
 FILE REFERENCE: AGENIX.051A  
 CURRENT APPLICATION NUMBER: US/10/041,860  
 CURRENT FILING DATE: 2002-01-07  
 NUMBER OF SEQ ID NOS: 377  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 225  
 LENGTH: 108  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-10-041-860-225

Query Match 100.0%; Score 558; DB 4; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-40;  
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQVSQSSYLAQKPGQAPRLIYATSSRATGIP 60  
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQVSQSSYLAQKPGQAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSGTDFTLTISRLPEPDAVYYCQYGSSPCSFSGQTKLRIK 108  
 Db 61 DRFGSGSGTDFTLTISRLPEPDAVYYCQYGSSPCSFSGQTKLRIK 108

RESULT 3  
 US-10-041-860-259  
 Sequence 259, Application US/10041860  
 Publication No. US20030157109A1  
 GENERAL INFORMATION:  
 APPLICANT: Corvalan, Jose R.F.  
 APPLICANT: Jia, Xiao-Chi  
 APPLICANT: Feng, Xiao  
 APPLICANT: Yang, Xiao-Dong  
 APPLICANT: Chen, Francine  
 APPLICANT: Gazit, Gadi  
 APPLICANT: Weber, Richard  
 APPLICANT: Bezabeh, Binyam  
 TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES  
 FILE REFERENCE: AGENIX.051A  
 CURRENT APPLICATION NUMBER: US/10/041,860  
 CURRENT FILING DATE: 2002-01-07  
 NUMBER OF SEQ ID NOS: 377  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 259  
 LENGTH: 108  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-10-041-860-259

Query Match 100.0%; Score 558; DB 4; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-40;  
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQVSQSSYLAQKPGQAPRLIYATSSRATGIP 60  
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQVSQSSYLAQKPGQAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSGTDFTLTISRLPEPDAVYYCQYGSSPCSFSGQTKLRIK 108  
 Db 61 DRFGSGSGTDFTLTISRLPEPDAVYYCQYGSSPCSFSGQTKLRIK 108

RESULT 4  
 US-10-041-860-375  
 Sequence 375, Application US/10041860  
 Publication No. US20030157109A1  
 GENERAL INFORMATION:  
 APPLICANT: Corvalan, Jose R.F.

RESULT 5  
 US-10-665-383-4  
 Sequence 4, Application US/10665383  
 Publication No. US20040141969A1  
 GENERAL INFORMATION:  
 APPLICANT: Floee, Juergen  
 APPLICANT: Gazit, Gadi  
 APPLICANT: Keyr, Bruce  
 APPLICANT: LaRochelle, William  
 APPLICANT: Lichtenstein, Henri  
 TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS  
 FILE REFERENCE: AGENIX.052A  
 CURRENT APPLICATION NUMBER: US/10/665,383  
 CURRENT FILING DATE: 2003-09-16  
 PRIOR APPLICATION NUMBER: 60/411,137  
 PRIOR FILING DATE: 2002-09-16  
 NUMBER OF SEQ ID NOS: 97  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 4  
 LENGTH: 108  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-10-665-383-4

Query Match 100.0%; Score 558; DB 4; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-40;  
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQVSQSSYLAQKPGQAPRLIYATSSRATGIP 60  
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQVSQSSYLAQKPGQAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSGTDFTLTISRLPEPDAVYYCQYGSSPCSFSGQTKLRIK 108  
 Db 61 DRFGSGSGTDFTLTISRLPEPDAVYYCQYGSSPCSFSGQTKLRIK 108

RESULT 6  
 US-10-891-658-84

Sequence 84, Application US/10891658  
 ; Publication No. US20050074821A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kenneth, Wild  
 ; APPLICANT: Treanor, James  
 ; APPLICANT: Huang, Haichun  
 ; APPLICANT: Inoue, Heather  
 ; APPLICANT: Zhang, Tie J.  
 ; APPLICANT: Martin, Frank  
 ; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway  
 ; FILE REFERENCE: 02-1240  
 ; CURRENT APPLICATION NUMBER: US/10/891,658  
 ; PRIORITY FILING DATE: 2004-07-15  
 ; PRIOR APPLICATION NUMBER: US 60/487,431  
 ; NUMBER OF SEQ ID NOS: 138  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 84  
 ; LENGTH: 108  
 ; TYPE: PRT  
 ; ORGANISM: homo sapien  
 ; US-10-891-658-84

Query Match 95.9%; Score 535; DB 5; Length 108;  
 Best Local Similarity 96.3%; Pred. No. 4.1e-38;  
 Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLISLSPGERATLSCRASQSSSSLYAQKPGQAPRLIYATSSRATGIP 60  
 Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSSSSLYAQKPGQAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSSGTDPLTISLSPPEFDAYYCQYGSSPCSGQGTKLEIK 108  
 Db 61 DRFGSGSSGTDPLTISLSPPEFDAYYCQYGSSPCSGQGTKLEIK 108

RESULT 7  
 US-10-891-658-131  
 ; Sequence 131, Application US/10891658  
 ; Publication No. US20050074821A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kenneth, Wild  
 ; APPLICANT: Treanor, James  
 ; APPLICANT: Huang, Haichun  
 ; APPLICANT: Inoue, Heather  
 ; APPLICANT: Zhang, Tie J.  
 ; APPLICANT: Martin, Frank  
 ; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway  
 ; FILE REFERENCE: 02-1240  
 ; CURRENT APPLICATION NUMBER: US/10/891,658  
 ; PRIORITY FILING DATE: 2004-07-15  
 ; PRIOR APPLICATION NUMBER: US 60/487,431  
 ; NUMBER OF SEQ ID NOS: 138  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 131  
 ; LENGTH: 108  
 ; TYPE: PRT  
 ; ORGANISM: homo sapien  
 ; US-10-891-658-131

Query Match 95.9%; Score 535; DB 5; Length 108;  
 Best Local Similarity 96.3%; Pred. No. 4.1e-38;  
 Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLISLSPGERATLSCRASQSSSSLYAQKPGQAPRLIYATSSRATGIP 60  
 Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSSSSLYAQKPGQAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSSGTDPLTISLSPPEFDAYYCQYGSSPCSGQGTKLEIK 108  
 Db 61 DRFGSGSSGTDPLTISLSPPEFDAYYCQYGSSPCSGQGTKLEIK 108

RESULT 8  
 US-10-910-901-18  
 ; Sequence 18, Application US/10910901  
 ; Publication No. US20050054019A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MICHAUD, NEIL R., et al.  
 ; TITLE OF INVENTION: ANTIBODIES TO c-NET  
 ; FILE REFERENCE: ABX-PFS  
 ; CURRENT APPLICATION NUMBER: US/10/910,901  
 ; CURRENT FILING DATE: 2004-08-03  
 ; PRIOR APPLICATION NUMBER: US 60/492,432  
 ; PRIOR FILING DATE: 2003-08-04  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn Ver. 3.2  
 ; SEQ ID NO: 18  
 ; LENGTH: 128  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-910-901-18

Query Match 95.9%; Score 535; DB 5; Length 128;  
 Best Local Similarity 96.3%; Pred. No. 4.8e-38;  
 Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLISLSPGERATLSCRASQSSSSLYAQKPGQAPRLIYATSSRATGIP 60  
 Db 21 EIVLTQSPGTLISLSPGERATLSCRASQSSSSLYAQKPGQAPRLIYATSSRATGIP 80

Qy 61 DRFGSGSSGTDPLTISLSPPEFDAYYCQYGSSPCSGQGTKLEIK 108  
 Db 81 DRFGSGSSGTDPLTISLSPPEFDAYYCQYGSSPCSGQGTKLEIK 128

RESULT 9  
 US-10-309-762-156  
 ; Sequence 156, Application US/10309762  
 ; Publication No. US20040018198A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gudasz, Jean  
 ; APPLICANT: Folitz, Ian  
 ; APPLICANT: Handa, Masahisa  
 ; APPLICANT: Gallo, Michael  
 ; TITLE OF INVENTION: CARBOXYIC ANHYDRASE IX  
 ; FILE REFERENCE: ABGENIX.027A  
 ; CURRENT APPLICATION NUMBER: US/10/309,762  
 ; PRIOR FILING DATE: 2001-12-03  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 156  
 ; LENGTH: 108  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-309-762-156

Query Match 95.5%; Score 533; DB 4; Length 108;  
 Best Local Similarity 95.4%; Pred. No. 6.1e-38;  
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLISLSPGERATLSCRASQSSSSLYAQKPGQAPRLIYATSSRATGIP 60  
 Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSSSSLYAQKPGQAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSSGTDPLTISLSPPEFDAYYCQYGSSPCSGQGTKLEIK 108  
 Db 61 DRFGSGSSGTDPLTISLSPPEFDAYYCQYGSSPCSGQGTKLEIK 108

RESULT 10  
 US-10-693-629-46  
 Sequence 4.6, Application US/10693629  
 Publication No. US20040120948A1  
 GENERAL INFORMATION:  
 APPLICANT: KIRIN BEER KABUSHIKI KAISHA  
 APPLICANT: MIKAYAMA, Toshihumi  
 APPLICANT: YOSHIDA, Hitoshi  
 APPLICANT: FORCE, Walker, R.  
 APPLICANT: CHEN, Xinsjie  
 APPLICANT: TAKAHASHI, Nobuaki  
 TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY  
 FILE REFERENCE: 021286-0306473  
 CURRENT APPLICATION NUMBER: US/10/693, 629  
 CURRENT FILING DATE: 2003-11-13  
 PRIOR APPLICATION NUMBER: PCT/US01/13672  
 PRIOR FILING DATE: 2001-04-27  
 PRIOR APPLICATION NUMBER: US/9/844, 684  
 PRIOR APPLICATION NUMBER: JP2001/142482  
 PRIOR FILING DATE: 2001-05-11  
 PRIOR APPLICATION NUMBER: JP2001/310535  
 PRIOR FILING DATE: 2001-04-27  
 PRIOR APPLICATION NUMBER: US/10/040, 244  
 PRIOR FILING DATE: 2001-10-05  
 NUMBER OF SEQ ID NOS: 66  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 46  
 LENGTH: 130  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-693-629-46

Query Match 95.4%; Score 533; DB 4; Length 130;  
 Best Local Similarity 95.4%; Pred. No. 7 3e-38;  
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQSSSYLAWYQKPGQAPRLIYATSSRATGIP 60  
 Db 21 BIVLTQSPGTLSLSPGERATLSCRASQSSSYLAWYQKPGQAPRLIYGASSRATGIP 80

Qy 61 DRFGSGSGTDPFLTISRLPEDFAYYCOQYGSPPCSFGQTKLEIK 108  
 Db 81 DRFGSGSGTDPFLTISRLPEDFAYYCOQYGSPTFGQTRLEIK 128

RESULT 11  
 US-10-307-724-123  
 Sequence 1.23, Application US/10307724  
 Publication No. US2003032972A1  
 GENERAL INFORMATION:  
 APPLICANT: Bowdish, Katherine S.  
 APPLICANT: Frederickson, Shana  
 APPLICANT: Renshaw, Mark  
 TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES  
 FILE REFERENCE: 1087-261P  
 CURRENT FILING DATE: 2002-12-02  
 PRIOR APPLICATION NUMBER: US 60/251, 448  
 PRIOR FILING DATE: 2000-12-05  
 PRIOR APPLICATION NUMBER: US 60/288, 889  
 PRIOR FILING DATE: 2001-05-04  
 PRIOR APPLICATION NUMBER: US 60/294, 068  
 PRIOR FILING DATE: 2001-05-29  
 NUMBER OF SEQ ID NOS: 193  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 123  
 LENGTH: 108  
 TYPE: PRT  
 ORGANISM: artificial sequence  
 FEATURE:

OTHER INFORMATION: antibody light chain variable region

US-10-737-290-123

Query Match 95.3%; Score 532; DB 5; Length 108;  
 Best Local Similarity 95.4%; Pred. No. 7.4e-38;  
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQSSSYLAWYQKPGQAPRLIYATSSRATGIP 60  
 Db 1 BIVLTQSPGTLSLSPGERATLSCRASQSSSYLAWYQKPGQAPRLIYGASSRATGIP 60

Qy 61 DRFGSGSGTDPFLTISRLPEDFAYYCOQYGSPPCSFGQTKLEIK 108  
 Db 61 DRFGSGSGTDPFLTISRLPEDFAYYCOQYGSPTFGQTRLEIK 108

RESULT 12  
 US-10-737-290-123  
 Sequence 1.23, Application US/10737290  
 Publication No. US2004025342A1  
 GENERAL INFORMATION:  
 APPLICANT: Bowdish, Katherine S.  
 APPLICANT: Frederickson, Shana  
 APPLICANT: Renshaw, Mark  
 APPLICANT: Orcencia, Cecilia  
 TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES  
 FILE REFERENCE: 1087-2 CIP III  
 CURRENT APPLICATION NUMBER: US/10/737, 290  
 CURRENT FILING DATE: 2003-12-15  
 PRIOR APPLICATION NUMBER: US 10/452, 590  
 PRIOR FILING DATE: 2003-06-02  
 PRIOR APPLICATION NUMBER: US 10/307, 724  
 PRIOR FILING DATE: 2002-12-02  
 PRIOR APPLICATION NUMBER: US 10/005, 593  
 PRIOR FILING DATE: 2001-12-05  
 PRIOR APPLICATION NUMBER: US 60/251, 448  
 PRIOR FILING DATE: 2000-12-05  
 PRIOR APPLICATION NUMBER: US 60/288, 889  
 PRIOR FILING DATE: 2001-05-04  
 PRIOR APPLICATION NUMBER: US 60/294, 068  
 PRIOR FILING DATE: 2001-05-29  
 NUMBER OF SEQ ID NOS: 193  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 123  
 LENGTH: 108  
 TYPE: PRT  
 ORGANISM: artificial sequence  
 FEATURE:

OTHER INFORMATION: antibody light chain variable region

US-10-737-290-123

Query Match 95.3%; Score 532; DB 5; Length 108;  
 Best Local Similarity 95.4%; Pred. No. 7.4e-38;  
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQSSSYLAWYQKPGQAPRLIYATSSRATGIP 60  
 Db 1 BIVLTQSPGTLSLSPGERATLSCRASQSSSYLAWYQKPGQAPRLIYGASSRATGIP 60

Qy 61 DRFGSGSGTDPFLTISRLPEDFAYYCOQYGSPPCSFGQTKLEIK 108  
 Db 61 DRFGSGSGTDPFLTISRLPEDFAYYCOQYGSPTFGQTRLEIK 108

RESULT 13  
 US-10-725-962-27  
 Sequence 2.7, Application US/10725962  
 Publication No. US20050013809A1  
 GENERAL INFORMATION:  
 APPLICANT: Samuel M. Owens  
 APPLICANT: Frank I. Carroll  
 APPLICANT: Phillip Abraham  
 APPLICANT: Melinda G. Gunnell

APPLICANT: Mary Haak-Frendsch  
 APPLICANT: Xiao Peng  
 TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE

FILE REFERENCE: ABEN01 071A  
 CURRENT APPLICATION NUMBER: US/10/725, 962  
 CURRENT FILING DATE: 2003-11-02  
 PRIOR APPLICATION NUMBER: 60/430717  
 PRIOR FILING DATE: 2002-12-02  
 NUMBER OF SEQ ID NOS: 141  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 27  
 LENGTH: 109  
 TYPE: PRT  
 ORGANISM: *Mus musculus*  
 US-10-725-962-27

Query Match 95.3%; Score 532; DB 5; Length 109;  
 Best Local Similarity 95.4%; Pred. No. 7.4e-38;  
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 EIVLTQSGTTLSPGERATLSCASQVSQSSYLAWTQKPCQAPRLIYATSSRATGIP 60  
 Qy 61 DRFGSGSGTDFLTISLEPEDFAVYCCQYGSPPCSFGQTKL8K 108

Db 61 DRFGSGSGTDFLTISLEPEDFAVYCCQYGSPPCSFGQTKV8K 108

RESULT 14  
 US-10-506-743-2  
 Sequence 2, Application US/10506743  
 Publication No. US2005010614041

GENERAL INFORMATION  
 APPLICANT: Lancaster, Joanne Sloan  
 TITLE OF INVENTION: Antagonistic Anti-hFas Ligand Human Antibodies and Fragments  
 TITLE OF INVENTION: Thereof  
 FILE REFERENCE: X15450 - National Stage  
 CURRENT APPLICATION NUMBER: US/10/506,743  
 CURRENT FILING DATE: 2004-09-03  
 PRIOR APPLICATION NUMBER: 60/367,054  
 PRIOR FILING DATE: 2002-03-21  
 NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 2  
 TYPE: PRT  
 ORGANISM: *Homo sapiens*  
 US-10-506-743-2

Query Match 95.3%; Score 532; DB 5; Length 120;  
 Best Local Similarity 95.4%; Pred. No. 8.2e-38;  
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 EIVLTQSGTTLSPGERATLSCASQVSQSSYLAWTQKPCQAPRLIYATSSRATGIP 60  
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Qy 61 DRFGSGSGTDFLTISLEPEDFAVYCCQYGSPPCSFGQTKL8K 108  
 Db 61 DRFGSGSGTDFLTISLEPEDFAVYCCQYGSPPCSFGQTKV8K 108

RESULT 15  
 US-10-737-290-161  
 Sequence 161, Application US/10737290  
 Publication No. US2004025324211  
 GENERAL INFORMATION  
 APPLICANT: Bowdish, Katherine S.  
 APPLICANT: Frederickson, Shana  
 APPLICANT: Renshaw, Mark  
 APPLICANT: Orencia, Cecilia  
 TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES

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OM protein - protein search, using sw model

Run on: May 15, 2006, 17:21:22 ; search time 17.1502 Seconds

(without alignments)  
295.651 Million cell updates/sec

Title: US-10-041-860-49

Perfect score: 558

Sequence: 1 BIVITQSPTLSLSPGERAT.....CQYQSSPCSFQGTKLKIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters:

250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing First 45 summaries

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12: /SIDSS5/podata/1/pubpa/US60\_NEW\_PUB.pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	ID	Description
1	530	95.0	384	11	US-11-00-463-804		Sequence 804, App
2	530	95.0	384	11	US-11-00-463-805		Sequence 805, App
3	530	95.0	384	11	US-11-00-463-806		Sequence 806, App
4	530	95.0	384	11	US-11-00-463-807		Sequence 807, App
5	529	94.8	109	9	US-10-834-397-16		Sequence 16, App
6	528	94.6	247	11	US-11-056-925-8		Sequence 8, App
7	528	94.6	249	11	US-11-056-925-4		Sequence 4, App
8	526	94.3	108	9	US-10-850-635-6		Sequence 6, App
9	525	94.2	131	9	US-10-721-733-27		Sequence 27, App
10	524	93.9	108	9	US-10-850-635-4		Sequence 4, App
11	524	93.9	108	11	US-11-051-633-58		Sequence 58, App
12	524	93.9	128	11	US-11-051-633-60		Sequence 60, App
13	523	93.7	108	10	US-11-211-917-113		Sequence 113, App
14	521	93.4	235	11	US-11-128-900-14		Sequence 14, App
15	521	93.4	235	11	US-11-128-900-65		Sequence 65, App
16	520	93.2	108	9	US-10-982-440-32		Sequence 32, App
17	520	93.2	108	9	US-10-982-440-36		Sequence 36, App
18	518	92.8	108	10	US-11-064-174-118		Sequence 178, App
19	514.5	92.2	113	11	US-11-049-536-104		Sequence 104, App
20	514.5	92.2	113	11	US-11-199-739-104		Sequence 60, App
21	513	91.9	291	11	US-11-041-095-60		Sequence 134, App

Sequence 134, App  
Sequence 74, App  
Sequence 332, App  
Sequence 334, App  
Sequence 168, App  
Sequence 1499, App  
Sequence 1264, App  
Sequence 1264, App  
Sequence 58, App  
Sequence 1219, App  
Sequence 1219, App  
Sequence 592, App  
Sequence 592, App  
Sequence 16, App  
Sequence 296, App  
Sequence 296, App  
Sequence 82, App  
Sequence 82, App  
Sequence 368, App  
Sequence 368, App  
Sequence 31, App  
Sequence 32, App

RESULT 1  
US-11-000-463-804

; Sequence 804, Application US/11000463

; Publication No. US2005266123A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Chen, Rui-hong B.

; APPLICANT: Qian, Xiaohong B.

; APPLICANT: Wang, Zhiwei

; APPLICANT: Wehrman, Tom

; APPLICANT: Zhang, Jie

; APPLICANT: Zhou, Ping

; APPLICANT: Cao, Yi-Cheng

; APPLICANT: Drmanac, Radivoje T.

; FILE REFERENCE: 755CPACN

; CURRENT APPLICATION NUMBER: US/11/000,463

; PRIOR APPLICATION NUMBER: 10/291,265

; PRIOR FILING DATE: 2002-11-08

; PRIOR APPLICATION NUMBER: PCT/US01/02623

; PRIOR FILING DATE: 2001-01-25

; PRIOR APPLICATION NUMBER: 09/922,279

; PRIOR FILING DATE: 2001-08-03

; PRIOR APPLICATION NUMBER: 09/491,404

; PRIOR FILING DATE: 2000-01-25

; PRIOR FILING DATE: 2000-07-17

; PRIOR APPLICATION NUMBER: 09/631,451

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: 09/633,870

; PRIOR FILING DATE: 2000-09-15

; NUMBER OF SEQ ID NOS: 944

; SOFTWARE: FastSEQ for Windows Version 3.0

; SBQ ID NO 804

; LENGTH: 384

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-11-000-463-804

Query Match Score 530; DB 11; Pred. No. 8.5e-37; Length 384;

; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 Query 1 EIVLTQSPGTLISLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYATSSRATGIP 60  
 Database 170 EIVLTQSPGTLISLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYGASSRATGIP 229

Query 61 DRFGSGSGGTDFLTISLRLPEDFAVYCCQYGSPPCSFGCGTKEIK 108  
 Database 230 DRFGSGSGGTDFLTISLRLPEDFAVYCCQYGSPPCSFGCGTKEIK 277

RESULT 2  
 US-11-000-463-805  
 Sequence 805, Application US/11000463  
 Publication No. US20050266423A1  
 GENERAL INFORMATION:  
 APPLICANT: Tang, Y. Tom  
 APPLICANT: Liu, Chenghua  
 APPLICANT: Asundi, Vinod  
 APPLICANT: Chen, Rui-hong B.  
 APPLICANT: Qian, Xiaohong B.  
 APPLICANT: Wang, Zhiwei  
 APPLICANT: Wehrman, Tom  
 APPLICANT: Zhang, Jie  
 APPLICANT: Zhou, Ping  
 APPLICANT: Cao, Yi-Cheng  
 APPLICANT: Dumanac, Radoe T.  
 TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
 FILE REFERENCE: 785C1P4CN  
 CURRENT APPLICATION NUMBER: US/11/000,463  
 PRIOR APPLICATION NUMBER: US/11/000,463  
 CURRENT FILING DATE: 2004-11-29  
 PRIOR APPLICATION NUMBER: 10/291,265  
 PRIOR FILING DATE: 2004-11-08  
 PRIOR APPLICATION NUMBER: PCT/US01/02623  
 PRIOR FILING DATE: 2001-01-25  
 PRIOR APPLICATION NUMBER: 09/922,279  
 PRIOR FILING DATE: 2001-08-03  
 PRIOR APPLICATION NUMBER: 09/491,404  
 PRIOR FILING DATE: 2000-01-25  
 PRIOR APPLICATION NUMBER: 09/617,746  
 PRIOR FILING DATE: 2000-07-17  
 PRIOR APPLICATION NUMBER: 09/631,451  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: 09/633,870  
 PRIOR FILING DATE: 2000-09-15  
 NUMBER OF SEQ ID NOS: 944  
 SEQ ID NO: 805  
 LENGTH: 384  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-000-463-806  
 Sequence 806, Application US/11000463  
 Publication No. US20050266423A1  
 GENERAL INFORMATION:  
 APPLICANT: Tang, Y. Tom  
 APPLICANT: Liu, Chenghua  
 APPLICANT: Asundi, Vinod  
 APPLICANT: Chen, Rui-hong B.  
 APPLICANT: Qian, Xiaohong B.  
 APPLICANT: Wang, Zhiwei  
 APPLICANT: Wehrman, Tom  
 APPLICANT: Zhang, Jie  
 APPLICANT: Zhou, Ping  
 APPLICANT: Cao, Yi-Cheng  
 APPLICANT: Dumanac, Radoe T.  
 TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
 FILE REFERENCE: 785C1P4CN  
 CURRENT APPLICATION NUMBER: US/11/000,463  
 PRIOR APPLICATION NUMBER: US/11/000,463  
 CURRENT FILING DATE: 2004-11-29  
 PRIOR APPLICATION NUMBER: 10/291,265  
 PRIOR FILING DATE: 2002-11-08  
 PRIOR APPLICATION NUMBER: PCT/US01/02623  
 PRIOR FILING DATE: 2001-01-25  
 PRIOR APPLICATION NUMBER: 09/922,279  
 PRIOR FILING DATE: 2001-08-03  
 PRIOR APPLICATION NUMBER: 09/491,404  
 PRIOR FILING DATE: 2000-01-25  
 PRIOR APPLICATION NUMBER: 09/617,746  
 PRIOR FILING DATE: 2000-07-17  
 PRIOR APPLICATION NUMBER: 09/631,451  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: 09/633,870  
 PRIOR FILING DATE: 2000-09-15  
 NUMBER OF SEQ ID NOS: 944  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 805  
 LENGTH: 384  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-000-463-805  
 Sequence 805, Application US/11000463  
 Publication No. US20050266423A1  
 GENERAL INFORMATION:  
 APPLICANT: Tang, Y. Tom  
 APPLICANT: Liu, Chenghua  
 APPLICANT: Asundi, Vinod  
 APPLICANT: Chen, Rui-hong B.  
 APPLICANT: Qian, Xiaohong B.  
 APPLICANT: Wang, Zhiwei  
 APPLICANT: Wehrman, Tom  
 APPLICANT: Zhang, Jie  
 APPLICANT: Zhou, Ping  
 APPLICANT: Cao, Yi-Cheng  
 APPLICANT: Dumanac, Radoe T.  
 TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
 FILE REFERENCE: 785C1P4CN  
 CURRENT APPLICATION NUMBER: US/11/000,463  
 PRIOR APPLICATION NUMBER: 10/291,265  
 PRIOR FILING DATE: 2002-11-08  
 PRIOR APPLICATION NUMBER: PCT/US01/02623  
 PRIOR FILING DATE: 2001-01-25  
 PRIOR APPLICATION NUMBER: 09/922,279  
 Query Match 1 EIVLTQSPGTLISLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYATSSRATGIP 60  
 Database 170 EIVLTQSPGTLISLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYGASSRATGIP 229  

RESULT 3  
 US-11-000-463-806  
 Sequence 806, Application US/11000463  
 Publication No. US20050266423A1  
 GENERAL INFORMATION:  
 APPLICANT: Tang, Y. Tom  
 APPLICANT: Liu, Chenghua

PRIOR FILING DATE: 2001-08-03  
 PRIOR APPLICATION NUMBER: 09/491,404  
 PRIOR FILING DATE: 2000-01-25  
 PRIOR APPLICATION NUMBER: US20000333A1  
 PRIOR FILING DATE: 2000-07-17  
 PRIOR APPLICATION NUMBER: 09/617,746  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: 09/631,451  
 PRIOR FILING DATE: 2000-09-15  
 PRIOR APPLICATION NUMBER: 09/633,870  
 NUMBER OF SEQ ID NOS: 944  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 807  
 LENGTH: 384  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-000-463-807

Query Match 95.0%; Score 530; DB 11; Length 384;  
 Best Local Similarity 94.4%; Pred. No. 8.5e-37;  
 Matches 1.02; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSIPLSPGERATLSRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60  
 Db 170 EIVLTQSPGTLSIPLSPGERATLSRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 229

Query Match 61 DRFGSGSGTGTDFLTISRLSPEDFAVYCCQYGSPCSFQGTKEIK 108  
 Best Local Similarity 94.4%; Pred. No. 8.5e-37;  
 Matches 1.02; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 61 DRFGSGSGTGTDFLTISRLSPEDFAVYCCQYGSPCSFQGTKEIK 108  
 Db 230 DRFGSGSGTGTDFLTISRLSPEDFAVYCCQYGSPCSFQGTKEIK 277

RESULT 5  
 Sequence 16, Application US/10834397  
 Publication No. US2006000333A1  
 GENERAL INFORMATION:  
 APPLICANT: Knappik, Achim  
 Pack, Peter  
 Flagg, Vic  
 Ge, Liming  
 Moroney, Simon  
 Plueckthun, Andreas  
 TITLE OF INVENTION: Protein/(poly)peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 ZIP: 10021  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/834,397  
 FILING DATE: 29-Apr-2004  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/490,324  
 FILING DATE: 24-Jan-2000  
 APPLICATION NUMBER: US/09/025,769  
 FILING DATE: 18-Feb-1998  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: James F. Haley, Jr., Esq.  
 REGISTRATION NUMBER: 27,794  
 PRIORITY/DOCKET NUMBER: MORPHO/5  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)596-9000  
 TELEFAX: (212)596-9090  
 INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 109 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: <Unknown>  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
 US-10-834-397-16

Query Match 94.8%; Score 529; DB 9; Length 109;  
 Best Local Similarity 94.4%; Pred. No. 3.4e-37;  
 Matches 1.02; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSIPLSPGERATLSRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60  
 Db 1 EIVLTQSPGTLSIPLSPGERATLSRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60

RESULT 6  
 Sequence 8, Application US/11056825  
 Publication No. US20050255109A1  
 GENERAL INFORMATION:  
 APPLICANT: Felding-Habermann, Brunhilde  
 APPLICANT: Janda, Kim D.  
 APPLICANT: Saven, Alan  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS  
 FILE REFERENCE: SCRP-0042  
 CURRENT APPLICATION NUMBER: US/11/056,825  
 CURRENT FILING DATE: 2005-02-11  
 PRIOR APPLICATION NUMBER: US 60/626,726  
 PRIOR FILING DATE: 2004-11-10  
 PRIOR APPLICATION NUMBER: US 60/544,807  
 PRIOR FILING DATE: 2004-02-13  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO: 8  
 LENGTH: 247  
 TYPE: PRT  
 ORGANISM: Artificial  
 FEATURE:  
 OTHER INFORMATION: Synthetic Construct  
 US-11-056-825-8

Query Match 94.6%; Score 528; DB 11; Length 247;  
 Best Local Similarity 94.4%; Pred. No. 8.5e-37;  
 Matches 1.02; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSIPLSPGERATLSRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60  
 Db 127 EIVLTQSPGTLSIPLSPGERATLSRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 186

Query Match 61 DRFGSGSGTGTDFLTISRLSPEDFAVYCCQYGSPCSFQGTKEIK 108  
 Best Local Similarity 94.4%; Pred. No. 8.5e-37;  
 Matches 1.02; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 61 DRFGSGSGTGTDFLTISRLSPEDFAVYCCQYGSPCSFQGTKEIK 108  
 Db 187 DRFGSGSGTGTDFLTISRLSPEDFAVYCCQYGSPCSFQGTKEIK 234

RESULT 7  
 Sequence 4, Application US/11056825  
 Publication No. US20050255109A1  
 GENERAL INFORMATION:  
 APPLICANT: Felding-Habermann, Brunhilde  
 APPLICANT: Janda, Kim D.  
 APPLICANT: Saven, Alan  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS  
 FILE REFERENCE: SCRP-0042  
 CURRENT APPLICATION NUMBER: US/11/056,825  
 CURRENT FILING DATE: 2005-02-11

FILE REFERENCE: PH-1573-PCT  
 CURRENT APPLICATION NUMBER: US/10/721,763  
 CURRENT FILING DATE: 2003-11-26  
 PRIORITY NUMBER: JP2001-150213  
 PRIORITY APPLICATION NUMBER: JP2001-05-18  
 PRIORITY FILING DATE: 2001-05-18  
 PRIORITY APPLICATION NUMBER: JP2001-243040  
 PRIORITY FILING DATE: 2001-08-09  
 PRIORITY APPLICATION NUMBER: JP2001-314489  
 PRIORITY FILING DATE: 2001-10-11  
 NUMBER OF SEQ ID NOS: 45  
 SEQ ID NO: 4  
 LENGTH: 249  
 TYPE: PRT  
 ORGANISM: Artificial  
 OTHER INFORMATION: Synthetic Construct  
 US-11-056-825-4

Query Match 94.6%; Score 528; DB 11; Length 249;  
 Best Local Similarity 94.4%; Pred. No. 8.5e-37;  
 Matches 102; Conservative 3; N mismatches 3; Indels 0; Gaps 0;  
 US-10-721-763-27

Query Match 94.2%; Score 525.5; DB 9; Length 131;  
 Best Local Similarity 95.4%; Pred. No. 7.8e-37;  
 Matches 104; Conservative 1; N mismatches 3; Indels 1; Gaps 1;  
 US-10-721-763-27

Query Match 94.2%; Score 525.5; DB 9; Length 131;  
 Best Local Similarity 95.4%; Pred. No. 7.8e-37;  
 Matches 104; Conservative 1; N mismatches 3; Indels 1; Gaps 1;

Query 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLLIYATSSRATGIP 60  
 Db 127 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLLIYATSSRATGIP 186  
 Query 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLLIYATSSRATGIP 60  
 Db 21 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLLIYATSSRATGIP 80  
 Query 61 DRFGSGSGTGTDTLTSRSLPEDFAVYCCQYGSPPRFQGKVDIK 234  
 Db 61 DRFGSGSGTGTDTLTSRSLPEDFAVYCCQYGSPPRFQGKVDIK 108  
 Query 81 DRFGSGSGTGTDTLTSRSLPEDFAVYCCQYGSPPRFQGKVDIK 129  
 Db 81 DRFGSGSGTGTDTLTSRSLPEDFAVYCCQYGSPPRFQGKVDIK 129

RESULT 10  
 Sequence 6, Application US/10850635  
 Publication No. US20050287149A1  
 PRIORITY NUMBER: US-10-850-635-4  
 Sequence 4, Application US/10850635  
 Publication No. US20050287149A1  
 GENERAL INFORMATION:  
 APPLICANT: Keler, Tibor  
 APPLICANT: Lowy, Israel  
 APPLICANT: Vitale, Laura  
 APPLICANT: Blanet, Diane  
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST  
 TITLE OF INVENTION: BACILLUS ANTHRACIS PROTECTIVE ANTIGEN  
 FILE REFERENCE: MXI-305  
 CURRENT APPLICATION NUMBER: US/10/850,635  
 CURRENT FILING DATE: 2004-05-21  
 PRIOR APPLICATION NUMBER: 60/472636  
 PRIOR FILING DATE: 2003-05-21  
 PRIOR APPLICATION NUMBER: 60/512336  
 PRIOR FILING DATE: 2003-10-16  
 NUMBER OF SEQ ID NOS: 72  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 6  
 LENGTH: 108  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-850-635-6

Query Match 94.3%; Score 526; DB 9; Length 108;  
 Best Local Similarity 95.4%; Pred. No. 6e-37;  
 Matches 103; Conservative 1; N mismatches 4; Indels 0; Gaps 0;  
 US-10-850-635-4

Query Match 93.9%; Score 524; DB 9; Length 108;  
 Best Local Similarity 94.4%; Pred. No. 8.8e-37;  
 Matches 102; Conservative 2; N mismatches 4; Indels 0; Gaps 0;

Query Match 93.9%; Score 524; DB 9; Length 108;  
 Best Local Similarity 94.4%; Pred. No. 8.8e-37;  
 Matches 102; Conservative 2; N mismatches 4; Indels 0; Gaps 0;

Query 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLLIYATSSRATGIP 60  
 Db 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLLIYATSSRATGIP 60  
 Query 61 DRFGSGSGTGTDTLTSRSLPEDFAVYCCQYGSPPRFQGKVDIK 108  
 Db 61 DRFGSGSGTGTDTLTSRSLPEDFAVYCCQYGSPPRFQGKVDIK 108  
 Query 61 DRFGSGSGTGTDTLTSRSLPEDFAVYCCQYGSPPRFQGKVDIK 108  
 Db 61 DRFGSGSGTGTDTLTSRSLPEDFAVYCCQYGSPPRFQGKVDIK 108

RESULT 11  
 Sequence 27, Application US/10721763  
 Publication No. US20050249729A1  
 GENERAL INFORMATION:  
 APPLICANT: KIRIN BEER KABUSHIKI KAISHA  
 TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY

GENERAL INFORMATION  
 APPLICANT: AMBROSINO, DONNA  
 APPLICANT: BABCOCK, GREGORY J.  
 APPLICANT: BROERTING, THERESE A.  
 APPLICANT: GHAZIANO, ROBERT  
 APPLICANT: HERNANDEZ, HECTOR JAVIER  
 APPLICANT: LOWY, ISRAEL  
 APPLICANT: MANDELLI, ROBERT  
 APPLICANT: MOLRINE, DEBORAH  
 APPLICANT: THOMAS, JR., WILLIAM D.  
 APPLICANT: ZHANG, HUI-PEN

TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: MJII-001  
 CURRENT APPLICATION NUMBER: US/11/051-453  
 CURRENT FILING DATE: 2005-02-04  
 PRIORITY NUMBER: 60/542,357  
 PRIOR FILING DATE: 2004-02-06  
 PRIORITY NUMBER: 60/613,854  
 PRIOR FILING DATE: 2004-09-28  
 NUMBER OF SEQ ID NOS: 82  
 SOFTWARE: PatentIn Ver. 3.3  
 SEQ ID NO: 58  
 LENGTH: 108  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-051-453-58

Query Match 93.9%; Score 524; DB 11; Length 108;  
 Best Local Similarity 94.4%; Pred. No. 8..8e-37;  
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 BIVLTQSGTTLISLSPGERATLSCRASQSSSYLAWYQQKPGQAPRILYATSSRATGIP 60  
 Db 1 BIVLTQSGTTLISLSPGERATLSCRASQSSSYLAWYQQKPGQAPRILYATSSRATGIP 60

Qy 61 DRFGSGSGTGTDTLISRLSPEDFAVYCCQYGSPPCSFGQGTKLTK 108  
 Db 61 DRFGSGSGTGTDTLISRLSPEDFAVYCCQQGSSTWTFGQTKVLIK 108

RESULT 12  
 US-11-051-453-60  
 ; Sequence 60, Application US/11051453  
 ; Publication No. US20050287150A1  
 ; GENERAL INFORMATION  
 ; APPLICANT: AMBROSINO, DONNA  
 ; APPLICANT: BABCOCK, GREGORY J.  
 ; APPLICANT: BROERTING, THERESE A.  
 ; APPLICANT: GHAZIANO, ROBERT  
 ; APPLICANT: HERNANDEZ, HECTOR JAVIER  
 ; APPLICANT: LOWY, ISRAEL  
 ; APPLICANT: MANDELLI, ROBERT  
 ; APPLICANT: MOLRINE, DEBORAH  
 ; APPLICANT: THOMAS, JR., WILLIAM D.  
 ; APPLICANT: ZHANG, HUI-PEN

TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: MJII-001  
 CURRENT APPLICATION NUMBER: US/11/051-453  
 CURRENT FILING DATE: 2005-02-04  
 PRIORITY NUMBER: 60/542,357  
 PRIOR FILING DATE: 2004-02-06  
 NUMBER OF SEQ ID NOS: 82  
 SOFTWARE: PatentIn Ver. 3.3  
 SEQ ID NO: 60  
 LENGTH: 128  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-051-453-60

Query Match 93.9%; Score 524; DB 11; Length 128;  
 Best Local Similarity 94.4%; Pred. No. 1e-36;  
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 BIVLTQSGTTLISLSPGERATLSCRASQSSSYLAWYQQKPGQAPRILYATSSRATGIP 60  
 Db 21 BIVLTQSGTTLISLSPGERATLSCRASQSSSYLAWYQQKPGQAPRILYATSSRATGIP 80

Qy 61 DRFGSGSGTGTDTLISRLSPEDFAVYCCQYGSPPCSFGQGTKLTK 108  
 Db 81 DRFGSGSGTGTDTLISRLSPEDFAVYCCQYGSSTWTFGQTKVLIK 128

RESULT 13  
 US-11-211-917-113  
 ; Sequence 113, Application US/112111917  
 ; Publication No. US20060093600A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BREDIAN, VAHE  
 ; APPLICANT: GLADUE, RONALD P.  
 ; APPLICANT: CORVALAN, JOSE  
 ; APPLICANT: JIA, XIAO-CHI  
 ; APPLICANT: BENG, XIAO  
 ; TITLE OF INVENTION: ANTIBODIES TO CD40  
 ; FILE REFERENCE: ABX-PF/3 US  
 ; CURRENT APPLICATION NUMBER: US/11/211,917  
 ; CURRENT FILING DATE: 2005-08-25  
 ; PRIORITY NUMBER: US/10/292,088  
 ; PRIOR FILING DATE: 2002-11-08  
 ; PRIORITY NUMBER: 60/348,980  
 ; PRIOR FILING DATE: 2001-11-09  
 ; NUMBER OF SEQ ID NOS: 147  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 113  
 ; LENGTH: 108  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-11-211-917-113

Query Match 93.7%; Score 523; DB 10; Length 108;  
 Best Local Similarity 93.5%; Pred. No. 1.1e-36;  
 Matches 101; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 BIVLTQSGTTLISLSPGERATLSCRASQSSSYLAWYQQKPGQAPRILYATSSRATGIP 60  
 Db 1 BIVLTQSGTTLISLSPGERATLSCRASQSSSYLAWYQQKPGQAPRILYATSSRATGIP 60

Qy 61 DRFGSGSGTGTDTLISRLSPEDFAVYCCQYGSPPCSFGQGTKLTK 108  
 Db 61 DRFGSGSGTGTDTLISRLSPEDFAVYCCQYGSSTWTFGQTKVLIK 108

RESULT 14  
 US-11-128-900-14  
 ; Sequence 14, Application US/11128900  
 ; Publication No. US20050287156A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HANSON, DOUGLAS C.  
 ; APPLICANT: NEVEU, MARK J.  
 ; APPLICANT: MOELLER, BILEEN E.  
 ; APPLICANT: HANKE, JEFFREY H.  
 ; APPLICANT: GILLMAN, STEVEN C.  
 ; APPLICANT: DAVIS, C. GEOFFREY  
 ; APPLICANT: CORVALAN, JOSE R.  
 ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
 ; FILE REFERENCE: ABX-PF/1 DIV3  
 ; CURRENT APPLICATION NUMBER: US/11/128,900  
 ; CURRENT FILING DATE: 2005-05-12  
 ; PRIORITY NUMBER: US 10/776549  
 ; PRIOR FILING DATE: 2004-02-10  
 ; PRIORITY NUMBER: US 10/612497  
 ; PRIOR APPLICATION NUMBER: 2003-07-01  
 ; PRIOR APPLICATION NUMBER: US 09/472087

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; PRIORITY FILING DATE: 1999-12-23
; PRIORITY APPLICATION NUMBER: US 60/113647
; PRIORITY FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 14
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-14

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Query Match          93.4%;  Score 521;  DB 11;  Length 235;
Best Local Similarity 91.7%;  Pred. No. 3.1e-36;
Matches 99;  Conservative 6;  Mismatches 3;  Indels 0;  Gaps 0;
Qy      1 BIVLTQSPGTLSLSPGERATLSCRAQSVSSELYQKRGQAPRLIYATSSRATGIP 60
Db      21 BIVLTQSPGTLSLSPGERATLSCRAQSISSSFLAMYQKRGQAPRLIYGASSRATGIP 80
Qy      61 DRFGSGSGGTDEFTLTISRLPEPDFAVYCCOYGSPPCSFGGTLEIK 108
Db      81 DRFGSGSGGTDEFTLTISRLPEPDFAVYCCOYGTSPWTFGGTKVIEK 128

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RESULT 15
US-11-128-900-65
Sequence 65, Application US/11128900
Publication No. US20050287136A1
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILEEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1.DIV3
CURRENT APPLICATION NUMBER: US/11/128,900
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: US 10/776649
PRIOR FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: US 10/612497
PRIOR APPLICATION NUMBER: 2003-07-01
PRIOR APPLICATION NUMBER: US 09/472087
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/113647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 65
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-11-128-900-65

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Query Match          93.4%;  Score 521;  DB 11;  Length 235;
Best Local Similarity 91.7%;  Pred. No. 3.1e-36;
Matches 99;  Conservative 6;  Mismatches 3;  Indels 0;  Gaps 0;
Qy      1 BIVLTQSPGTLSLSPGERATLSCRAQSVSSELYQKRGQAPRLIYATSSRATGIP 60
Db      21 BIVLTQSPGTLSLSPGERATLSCRAQSISSSFLAMYQKRGQAPRLIYGASSRATGIP 80
Qy      61 DRFGSGSGGTDEFTLTISRLPEPDFAVYCCOYGSPPCSFGGTLEIK 108
Db      81 DRFGSGSGGTDEFTLTISRLPEPDFAVYCCOYGTSPWTFGGTKVIEK 128

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Result No.	Score	Query Match	Length	DB ID	Description
1	535	95.9	108	C30608	Ig kappa chain V-I
2	535	95.9	109	H30601	Ig kappa chain V-I
3	534	95.7	109	P30601	Ig kappa chain V-I
4	533	95.5	109	B30601	Ig kappa chain V-I
5	531	95.2	109	PH0963	Ig kappa chain V-I
6	531	95.2	109	D30601	Ig kappa chain V-I
7	530	95.0	109	C30601	Ig kappa chain V-I
8	530	95.0	129	2	Ig light chain var
9	530	95.0	134	2	Ig kappa chain V-I
10	529	94.8	109	2	Ig kappa chain V-I
11	529	94.8	129	2	Ig kappa chain V-I
12	528	94.6	129	1	K3H0H1
13	527	94.4	128	2	S20636
14	526	94.3	129	1	K3H0H1
15	524	93.9	109	1	K3H0H1
16	524	93.9	109	1	F30601
17	523.5	93.8	114	2	S46307
18	521	93.4	109	1	K3H0H1
19	520	93.2	109	2	A30608
20	515	92.3	109	2	G30607
21	514	92.1	107	2	PH0965
22	514	92.1	108	2	B30608
23	513	91.9	124	2	S20633
24	511	91.6	121	2	S40327
25	508	91.0	109	1	K3H0H1
26	507	90.9	110	2	S20635
27	504.5	90.4	108	2	E30609
28	503.5	90.2	110	2	E30607
29	503	90.1	108	1	K3H0H1

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin <IMM>  
 F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.9%; Score 535; DB 2; Length 109;  
 Best Local Similarity 96.3%; Pred. No. 3.8e-38;  
 Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYATSSRATGIP 60  
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYGASSRATGIP 60

Qy 61 DRFGSGSGTDFLTLSRLEPEDFAVYQCGYSSPCSFQGQTKLEIK 108  
 Db 61 DRFGSGSGTDFLTLSRLEPEDFAVYQCGYSSPCSFQGQTKLEIK 108

RESULT 3

F30601 Ig kappa chain V-III region (Neu) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 21-Jan-2000  
 C;Accession: F30601  
 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo J.; Immunol., 142, 3158-3163, 1989  
 A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies: heterotetramer; immunoglobulin homology <IMM>  
 A;Reference number: A30601; MUID:89215279; PMID:2496160  
 A;Accession: F30601  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Keywords: heterotetramer; immunoglobulin homology <IMM>  
 F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.7%; Score 534; DB 2; Length 109;  
 Best Local Similarity 93.5%; Pred. No. 4.6e-38;  
 Matches 101; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYATSSRATGIP 60  
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYGASSRATGIP 60

Qy 61 DRFGSGSGTDFLTLSRLEPEDFAVYQCGYSSPCSFQGQTKLEIK 108  
 Db 61 DRFGSGSGTDFLTLSRLEPEDFAVYQCGYSSPCSFQGQTKLEIK 108

RESULT 6

D30601 Ig kappa chain V-III region (Cur) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
 C;Accession: D30601  
 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo J.; Immunol., 142, 3158-3163, 1989  
 A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies: heterotetramer; immunoglobulin homology <IMM>  
 A;Reference number: A30601; MUID:89215279; PMID:2496160  
 A;Accession: D30601  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Keywords: heterotetramer; immunoglobulin homology <IMM>

Query Match 95.2%; Score 531; DB 2; Length 109;  
 Best Local Similarity 95.4%; Pred. No. 8.2e-38;  
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYATSSRATGIP 60  
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYGASSRATGIP 60

RESULT 4

B30601 Ig kappa chain V-III region (Glo) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
 C;Accession: B30601  
 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo J.; Immunol., 142, 3158-3163, 1989  
 A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies: heterotetramer; immunoglobulin homology <IMM>  
 A;Reference number: A30601; MUID:89215279; PMID:2496160  
 A;Accession: B30601  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Keywords: heterotetramer; immunoglobulin homology <IMM>

Query Match 95.5%; Score 533; DB 2; Length 109;  
 Best Local Similarity 95.4%; Pred. No. 5.6e-38;  
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYATSSRATGIP 60  
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYGASSRATGIP 60

Qy 61 DRFGSGSGTDTPLTISRLPEDFAVYCCQYGSSPCSGQGTTKLEIK 108  
 Db 61 DRFGSGSGTDTPLTISRLPEDFAVYCCQYGSSPCSGQGTTKLEIK 108

RESULT 7  
 C30601  
 C;Species: Homo sapiens (man)  
 C;Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
 C;Accession: C30601  
 R;Goni, P.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Carson, D.; Soldi, J.; Immunol. 142, 3158-3163, 1989  
 A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies  
 A;Reference number: A30601; MUID:89215279; PMID:2496160  
 A;Accession: C30601  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-109 <CON>  
 A;Cross-references: UNIPROT:Q9UJ78; UNIPARC:UPI0000176AEB  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 109;  
 Best Local Similarity 94.4%; Pred. No. 9.9e-38; Indels 0; Gaps 0;  
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 BIVLQSPGTLSLSPGERATLSCRASQSVSSYLLWQKPGQAPRLIYATSSRATGIP 60  
 Db 1 BIVLQSPGTLSLSPGERATLSCRASQSVSSYLLWQKPGQAPRLIYASSRATGIP 60

Qy 61 DRFGSGSGTDTPLTISRLPEDFAVYCCQYGSSPCSGQGTTKLEIK 108  
 Db 61 DRFGSGSGTDTPLTISRLPEDFAVYCCQYGSSPCSGQGTTKLEIK 108

RESULT 8  
 S46369  
 IG light chain variable region (VJ) - human  
 C;Species: Homo sapiens (man)  
 C;Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
 C;Accession: S46369  
 R;Bensimon, C.; Chastagner, P.; Zouali, M.  
 EMB J. 13, 2951-2962, 1994  
 A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rearrangement  
 A;Reference number: S46369; MUID:94131975; PMID:8039491  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-129 <BEN>  
 A;Cross-references: UNIPARC:UPI0000176CA5; EMBL:227170  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: immunoglobulin  
 F;36-111/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 129;  
 Best Local Similarity 95.4%; Pred. No. 1.2e-37; Indels 0; Gaps 0;  
 Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 BIVLQSPGTLSLSPGERATLSCRASQSVSSYLLWQKPGQAPRLIYATSSRATGIP 60  
 Db 21 BIVLQSPGTLSLSPGERATLSCRASQSVSSYLLWQKPGQAPRLIYASSRATGIP 80

Qy 61 DRFGSGSGTDTPLTISRLPEDFAVYCCQYGSSPCSGQGTTKLEIK 108  
 Db 81 DRFGSGSGTDTPLTISRLPEDFAVYCCQYGSSPCSGQGTTKLEIK 128

RESULT 9  
 S38643  
 Ig kappa chain V region - human (fragment)  
 C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C;Accession: S38643  
 R;Bensimon, C.; Chastagner, P.; Zouali, M.  
 Submitted to the EMBL Data Library, November 1993  
 A;Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.  
 A;Accession: S38643  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-134 <BEN>  
 A;Cross-references: UNIPARC:UPI00001165A2; EMBL:227170; NID:9415955; PIDN:CAA81694.1; PI  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;41-116/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 134;  
 Best Local Similarity 95.4%; Pred. No. 1.2e-37; Indels 0; Gaps 0;  
 Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 BIVLQSPGTLSLSPGERATLSCRASQSVSSYLLWQKPGQAPRLIYATSSRATGIP 60  
 Db 26 BIVLQSPGTLSLSPGERATLSCRASQSVSSYLLWQKPGQAPRLIYASSRATGIP 85

Qy 61 DRFGSGSGTDTPLTISRLPEDFAVYCCQYGSSPCSGQGTTKLEIK 108  
 Db 86 DRFGSGSGTDTPLTISRLPEDFAVYCCQYGSSPCSGQGTTKLEIK 133

RESULT 10  
 G30601  
 Ig kappa chain V-III region (Got) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
 C;Accession: G30601  
 R;Goni, P.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Carson, D.; Solc J.; Immunol. 142, 3158-3163, 1989  
 A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies  
 A;Reference number: A30601; MUID:89215279; PMID:2496160  
 A;Accession: G30601  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-109 <CON>  
 A;Cross-references: UNIPROT:Q9UJ78; UNIPARC:UPI0000176AEB  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 529; DB 2; Length 109;  
 Best Local Similarity 95.4%; Pred. No. 1.2e-37; Indels 0; Gaps 0;  
 Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 BIVLQSPGTLSLSPGERATLSCRASQSVSSYLLWQKPGQAPRLIYATSSRATGIP 60  
 Db 1 BIVLQSPGTLSLSPGERATLSCRASQSVSSYLLWQKPGQAPRLIYASSRATGIP 60

Qy 61 DRFGSGSGTDTPLTISRLPEDFAVYCCQYGSSPCSGQGTTKLEIK 108  
 Db 61 DRFGSGSGTDTPLTISRLPEDFAVYCCQYGSSPCSGQGTTKLEIK 108

RESULT 11  
 S49532  
 anti-Sm antibody VI chain (V kappa 3/J kappa 2) - human  
 C;Species: Homo sapiens (man)  
 C;Date: 01-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 21-Jan-2000  
 C;Accession: S49532  
 R;Malmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.  
 Submitted to the EMBL Data Library, October 1994  
 A;Description: Molecular characterization of natural human anti-Sm autoantibodies.  
 A;Reference number: S48797  
 A;Accession: S49532  
 A;Status: preliminary  
 A;Molecule type: mRNA

A;Residues: 1-129 <NAH>			
A;Cross-references: UNIPARC:UPI00001166FC; EMBL:Z46345; NID:9560843; PIDN:CAA86464-1; PI			
C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>			
F;36-111;Domain: immunoglobulin homology <IMM>			
Query Match 94.6%; Score 529; DB 2; Length 129;			
Best Local Similarity 95.4%; Pred. No. 1.4e-3;			
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;			
Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQSVSSYSLWYQKPGQAPRLLIYATSSRATGIP 60			
Db 21 BIVLTQSPGTLSLSPGERATLSCRASQSVSSYSLWYQKPGQAPRLLIYGASSRATGIP 80			
Qy 61 DRFGSGSGSGTGTDFLTLSRLEPEDFAVYTCQOYQSSPCSFQGQTKLEIK 108			
Db 81 DRFGSGSGSGTGTDFLTLSRLEPEDFAVYTCQOYQSSPQFGQGQTKLEIK 128			
RESULT 12			
K3H0HA			
Ig kappa chain precursor V-III region (Hah) - human			
C;Species: Homo sapiens (man)			
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004			
C;Accession: Pj0022			
R;KIPPS, T.J.; Tomhave, B.; Chen, P.P.; Carson, D.A.			
J. J. Exp. Med. 167, 840-852, 1988			
A;Title: Autoantibody-associated kappa light chain variable region gene expressed in ch			
C;Genetics: A;Reference number: PL0021; MUID:88171307; PMID:3127527			
A;Molecule type: mRNA			
A;Residues: 1-129 <NAH>			
A;Cross-references: UNIPROT:PI18135; UNIPARC:UPI000012E163			
C;Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed in			
C;Genetics:			
A;Gene: GRB; IGRV3			
A;Cross-references: GDB:136266			
A;Map Position: 2p12-2p11			
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κ) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la			
C;Superfamily: immunoglobulin V region; immunoglobulin homology			
C;Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin			
F;1-20/Domain: Signal sequence #status predicted <SG>			
F;21-129/Domain: Product: Ig kappa chain V-III region (Hah) #status predicted <MAT>			
F;21-117/Region: V segment			
F;36-111;Domain: immunoglobulin homology <IMM>			
F;44-55/Region: complementarity-determining 1			
F;71-77/Region: complementarity-determining 2			
F;110-117/Region: J segment (JKL)			
F;118-129/Region: J segment (JKL)			
F;43-109/Disulfide bonds: #status predicted			
Query Match 94.6%; Score 528; DB 1; Length 129;			
Best Local Similarity 94.4%; Pred. No. 1.7e-37;			
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;			
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Db 21 BIVLTQSPGTLSLSPGERATLSCRASQSVSSYSLWYQKPGQAPRLLIYGASSRATGIP 80			
Qy 61 DRFGSGSGSGTGTDFLTLSRLEPEDFAVYTCQOYQSSPCSFQGQTKLEIK 108			
Db 81 DRFGSGSGSGTGTDFLTLSRLEPEDFAVYTCQOYQSSPQFGQGQTKLEIK 128			
RESULT 13			
S20636			
Ig kappa chain V region - human			
C;Species: Homo sapiens (man)			
C;Accession: S20636			
R;Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.			
A;Submitted to the EMBL Data Library, April 1992			
A;Reference number: S20631			

C;Accession: A01895  
R;Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.  
Hoppe-Seyler, S. Z. Physiol. Chem. 353, 189-208, 1972  
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-kette vom kappa-Typ, Sub  
A;Reference: number: A91651; MUID:72188439; PMID:5027703  
A;Accession: A01895  
A;Molecule type: protein  
A;Residues: 1-109 <sum>  
A;Cross-references: UNIPROT:P01622; UNIPARC:UPI000012E15D  
A;Note: the sequence of the C region, which has the Inv (3) marker, is also given  
C;Comment: This is a Bence Jones protein.  
C;Genetics:  
A;Gene: GDB:IGKV3  
A;Cross-references: GDB:136266  
A;Map position: 2p12-2p11  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer  
P;16-91/Domain: immunoglobulin homology <IMM>  
P;23-89/Disulfide bonds: #status predicted  
A;Map position: 2p12-2p11  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer  
P;16-91/Domain: immunoglobulin homology <IMM>  
P;23-89/Disulfide bonds: #status predicted

Query Match 93.9%; Score 524; DB 1; Length 109;  
Best Local Similarity 92.6%; Pred. No. 3.2e-37;  
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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Qy	61 DRFGSGSGGTDFPLTISRLPEPDFAVYCCOYGSSPCSFQGQTKLRLIK 108	Db	61 DRFGSGSGGTDFPLTISRLPEPDFAVYCCQGSSPFQGQTKLVLK 108

Search completed: May 15, 2006, 17:04:49  
Job time : 22.7854 secs

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GenCore version 5.1.8	May 15, 2006, 16:54:27 ; Search time 138.592 Seconds	2166443	2166443 seqs, 705528306 residues	2166443
Copyright (c) 1993 - 2006 Biocceleration Ltd.	(without alignments)			
4 protein - protein search, using SW mode	549.793 Million cell updates/sec			
run on:	May 15, 2006, 16:54:27 ; Search time 138.592 Seconds			
post-processing:	Minimum Match 0%			
	Maximum Match 100%			
	Listing first 45 summaries			
database :	Uniprot_05_80:*			
	1: uniprot_sprot:*			
	2: uniprot_trembl:*			
scoring table:	BLOSUM62			
gapopen:	10.0			
gapext:	0.5			
searched:	2166443 seqs, 705528306 residues			
Total number of hits satisfying chosen parameters:	2166443			
Maximum DB seq length: 0				
Maximum DB seq length: 2000000000				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
result No.	Score	Query	Match	Length
				DB ID
1	528	94.6	129	1 KV3L_HUMAN
2	526	94.3	129	1 KV3M_HUMAN
3	524	93.9	109	1 KV3D_HUMAN
4	521	93.4	109	1 KV3B_HUMAN
5	518	92.8	109	2 Q9UJ78_HUMAN
6	508	91.0	109	1 KV3E_HUMAN
7	506.5	90.8	236	2 Q6P1L8_HUMAN
8	504	90.3	109	2 Q9UJ86_HUMAN
9	503	90.1	108	1 KV3A_HUMAN
10	500	89.6	109	1 KV3G_HUMAN
11	493	88.4	235	2 Q6P1F2_HUMAN
12	491	88.0	235	2 Q6GMV9_HUMAN
13	481.5	86.3	236	2 Q6P5S8_HUMAN
14	466	83.5	100	1 KV3C_HUMAN
15	465.5	83.4	128	1 KV3K_HUMAN
16	446	79.9	109	1 KV3F_HUMAN
17	445.5	79.8	234	2 Q563T9_HUMAN
18	439	78.7	129	1 KV3H_HUMAN
19	435.5	78.0	129	1 KV3I_HUMAN
20	426	76.3	109	2 Q9UL85_HUMAN
21	420.5	75.4	115	1 KV3J_HUMAN
22	420	75.3	135	2 Q6GRW0_HUMAN
23	415.5	74.5	114	1 KV4A_HUMAN
24	414	74.2	116	1 KV3J_HUMAN
25	399.5	71.6	134	1 KV4C_HUMAN
26	398.5	71.4	108	2 Q9UL79_HUMAN
27	397.5	71.2	108	1 KV1H_HUMAN
28	394.5	71.0	236	2 Q6P1H7_HUMAN
29	390.5	70.0	108	2 Q9UL77_HUMAN
30	388.5	69.4	133	2 KV4B_HUMAN
31	386.5	69.3	108	2 Q9UL78_HUMAN
32	386.5	69.3	236	2 Q6GMX8_HUMAN
33	384	68.8	114	2 Q8K1F1_mus_musculu
34	383.5	68.7	131	2 Q811C3_mus_musculu
35	382.5	68.5	108	1 KV1M_HUMAN
36	382.5	68.5	236	2 Q7Z3T4_HUMAN
37	382.5	68.5	236	2 Q6GMX9_HUMAN
38	381.5	68.4	244	2 Q652C8_HUMAN
39	381	68.3	107	2 Q965A9_HUMAN
40	380.5	68.2	108	1 KV1F_HUMAN
41	379.5	68.0	108	1 KV1K_HUMAN
42	378.5	67.8	234	2 Q7Z4T3_HUMAN
43	377.5	67.7	240	2 Q6P1T5_HUMAN
44	377.5	67.7	240	2 Q652C9_HUMAN
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SQ	SEQUENCE	129 AA;	14073 MW;	D3CS5292772774D0	CRC64;	Matches	102;	Conservative	2;	Mismatches	4;	Indels	0;	Gaps	0;
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Matches 102;	Conservative	3;	Mismatches	3;	Indels 0;	Gaps 0;									
Qy	1	BIVLTQSPETLSSLSPGERATLSCRAQSVSSESYLAWQOKPQAPRLLIYATSSRATGIP	60												
Db	21	BIVLTQSPETLSSLSPGERATLSCRAQSVSSESYLAWQOKPQAPRLLIYATSSRATGIP	60												
Qy	61	DRFSGSGSGTDFLTISRLPEPDFAVYCCQYGSPPSFQGTKEIK	108												
Db	81	DRFSGSGSGTDFLTISRLPEPDFAVYCCQYGSPPSFQGTKEIK	128												
	RESULT 3														
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ID	KV3D_HUMAN	STANDARD;													
AC	P01622;														
DT	21-JUL-1986	(Rel. 01, Created)													
DT	21-JUL-1986	(Rel. 01, Last sequence update)													
DT	10-MAY-2005	(Rel. 47, Last annotation update)													
DB	19 kappa chain V-III region Ti.														
OS	Homo sapiens (Human).														
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;														
OC	Homo sapiens (Human).														
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;														
OC	Homo sapiens (Human).														
OX	NCBI_TaxID=9606;														
RN															
RN	[1]														
RN	NUCLEOTIDE SEQUENCE.														
RX	DOI=10.1084/jem.167.3.840;														
RA	01-NOV-1990 (Rel. 16, Created).														
DT	01-NOV-1990 (Rel. 16, Last sequence update)														
DT	01-MAY-2005 (Rel. 47, Last annotation update)														
DE	19 kappa chain V-III region HIC precursor.														
DE	Homo sapiens (Human).														
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;														
CC	Homo sapiens (Human).														
CC	NCBI_TaxID=9606;														
CC	NUCLEOTIDE SEQUENCE.														
RX	DOI=10.1084/jem.167.3.840;														
RA	01-NOV-1990 (Rel. 16, Created).														
DT	01-NOV-1990 (Rel. 16, Last sequence update)														
DE	19 kappa chain V-III region HIC precursor.														
DE	Homo sapiens (Human).														
CC	KiPPs T.J., Tomhive E., Chen P.P.; Carson D.A.;														
CC	"Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy."														
RL	J. EXP. MED. 167:840-852 (1988).														
CC	-1- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.														
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.														
CC	PIR; P01621; K3HUHI.														
CC	HSSP; P01625; IEEQ.														
CC	SMR; P18136; 21-129.														
CC	Ensembl; ENSG00000169769; Homo sapiens.														
CC	GO; GO:0003823; F: extracellular region; NAS.														
CC	GO; GO:006955; P: immune response; NAS.														
CC	InterPro; IPR007110; Ig-like.														
CC	InterPro; IPR003596; Ig_Y.														
CC	SMART; SM0006; Ig_V.														
CC	PROSITE; PS00835; Ig_LIKE.														
CC	Immunoglobulin domain; Immunoglobulin V region; Signal.														
CC	SIGNAL	1	20												
FT	CHAIN	21	129												
FT	REGION	21	43												
FT	REGION	44	55												
FT	REGION	56	70												
FT	REGION	71	77												
FT	REGION	78	109												
FT	REGION	110	118												
FT	REGION	119	129												
FT	DISULFID	43	109												
FT	NON_TER	129	129												
SQ	SEQUENCE	129 AA;	14071 MW;	7395528EA2BB74D6	CRC64;	Query Match	93.9%	Score 524;	DB 1;	Length 109;					
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FT	SEQUENCE	1	BIVLTQSPETLSSLSPGERATLSCRAQSVSSESYLAWQOKPQAPRLLIYATSSRATGIP	60		Best Local Similarity	92.6%;	Pred. No. 1	5e-4						
FT	SEQUENCE	1	EIVLTQSPETLSSLSPGERATLSCRAQSVSSESYLAWQOKPQAPRLLIYATSSRATGIP	80		FT	SEQUENCE	109 AA;	11788 MW;	8C35055CDC7749BC CRC64;	FT	SEQUENCE	109 AA;	11788 MW;	8C35055CDC7749BC CRC64;
FT	SEQUENCE	1	DRFSGSGSGTDFLTISRLPEPDFAVYCCQYGSPPSFQGTKEIK	108		Query Match	93.9%;	Score 524;	DB 1;	Length 109;					
FT	SEQUENCE	1	DRFSGSGSGTDFLTISRLPEPDFAVYCCQYGSPPSFQGTKEIK	128		Best Local Similarity	92.6%;	Pred. No. 1	5e-4						
FT	SEQUENCE	1	DRFSGSGSGTDFLTISRLPEPDFAVYCCQYGSPPSFQGTKEIK	108		FT	SEQUENCE	109 AA;	11788 MW;	8C35055CDC7749BC CRC64;	FT	SEQUENCE	109 AA;	11788 MW;	8C35055CDC7749BC CRC64;
FT	SEQUENCE	1	DRFSGSGSGTDFLTISRLPEPDFAVYCCQYGSPPSFQGTKEIK	128		Query Match	94.3%;	Score 526;	DB 1;	Length 129;					
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RESULT 11		Q6PF2 HUMAN PRELIMINARY;		PRT;		235 AA.	
ID	Q6PF2	HUMAN PRELIMINARY;					
AC	Q6PF2_	HUMAN PRELIMINARY;					
DT	05-JUL-2004	(TREMBLrel. 27, Created)					
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)					
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)					
DE	Hypothetical protein.						
OS	Homo sapiens (Human)						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.						
NCBI_TaxID	9606;						
OX							
RN							
RC							
RC		NUCLEOTIDE SEQUENCE.					
RC		TISSUE=Lung;					
RX		MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;					
RA		Strausberg R.L., Feingold B.A., Grouse L.H., Degege J.G.,					
RA		Klaunser R.D., Collins F.S., Wagner L., Shevchenko C.M., Schuler G.D.,					
RA		Altenschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F.,					
RA		Hopkins N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Hsieh F.,					
RA		Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,					
RA		Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,					
RA		Brownstein M.J., Ustain T.B., Toshiyuki S., Carninci P., Prange C.,					
RA		Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,					
RA		Richards S., Worley K.C., Hale S., Garcia A.M., Soderberg D.M., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergran B.J., Gay J.B., Hulyk S.W.,					
RA		Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Rodriguez S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,					
RA		Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,					
RA		Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,					
RA		"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";					
RA		RT					
RA		RT					
RA		RT					
RA		RL					
RN							
RC		NUCLEOTIDE SEQUENCE.					
RC		TISSUE=Lung;					
RA		Strausberg R.J.					
RL		Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.					
DR		EMBL; BC016380; AAH16380.1; -; mRNA.					
DR		HSSP; P01837; 1KCU.					
DR		SMR; Q6PF2;					
DR		DR; Q6PF2; 21-235.					
DR		InterPro; IPR003599; Ig.					
DR		InterPro; IPR007110; Ig-like.					
DR		InterPro; IPR003597; Ig-cl.					
DR		InterPro; IPR00306; Ig_MHC.					
DR		InterPro; IPR003596; Ig_v.					
DR		InterPro; IPR003596; Ig_y.					
DR		Pfam; PF07654; Cl-set; 1.					
DR		SMART; SM00409; Ig; 2.					
DR		SMART; SM00407; IgCl1.					
DR		SMART; SM00446; IgV; 1.					
DR		PROSITE; PS50835; Ig_LIKE; 2.					
DR		PROSITE; PS00290; Ig_MHC; UNKNOWN_1.					
KW		Hypothetical protein.					
SQ		SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;					
Query		Match	88.4%	Score	493;	DB 2;	Length 235;
Best		Local Similarity	88.0%	Pred. No.	6e-43;		
Matches		95;	Conservative	7;	Mismatches	6;	Indels 0;
Db		1	EIVLTQSPGTLSLSPGERATLSCRASVSSSYLWYQKIQGAPLLIYATSSRATGIP	60			
Db		21	EIVLTQSPGTLSLSPGERATLSCRASVSSSYLWYQKIQGAPLLIYATSSRATGIP	80			
Qy		61	DRFGSGSGGTDTFLTISRLPEPDEVYYCQGYGSSPCSGTGTGKIK	108			
Db		81	DRFGSGSGGTDTFLTISRLPEPDEVYYCQGYGSSPCSGTGTGKIK	128			

RESULT 13  
Q6PS88\_HUMAN

ID	Q6P5SB	HUMAN PRELIMINARY;	PRT;	236 AA.	AC	P01621;	DT 21-JUL-1986 (Rel. 01, Created)
DR	05-JUL-2004	(TREMBLrel. 27, Created)			DT	21-JUL-1986 (Rel. 01, Last sequence update)	
DR	05-JUL-2004	(TREMBLrel. 27, Last sequence update)			DT	10-MAY-2005 (Rel. 47, Last annotation update)	
DB	Hypothetical protein.				DS	19 kappa chain V-III region N69 precursor (fragment).	
OS	Homo sapiens (Human).				OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.				OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.	
OC					OC		
OC					OC		
OX	NCBI_TAXID=9606;				OX	NCBI_TAXID=9606;	
RN	[1]				RN	[1]	
RP	NUCLEOTIDE SEQUENCE.				RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE-Glandular pool- thyroid;				RX	MEDLINE=84093600; PubMed=6419127;	
RX	MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;				RA	Bentley D.L.;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				RT	"Most kappa immunoglobulin mRNA in human lymphocytes is homologous to a small family of germ-line V genes.";	
RA	Klausner R.D., Collins P.S., Wagner L., Shemesh C.M., Schuler G.D.,				RL	Nature 307:780 (1984).	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				CC	-1 - MISCELLANEOUS: This gene was isolated from the NG9/9.1 hybridoma.	
RA	Dapchankov L., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.	
RA	Stapleton M., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				CC		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				CC		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,				CC		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				CC		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				CC		
RA	Villanueva D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				CC		
RA	Fahey J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,				CC		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				CC		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				CC		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				CC		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,				CC		
RA	Schnecher A., Schein J.B., Jones S.J.M., Marra M.A.,				CC		
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";				CC		
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).				CC		
RN	[2]				CC		
RC	NUCLEOTIDE SEQUENCE.				CC		
RA	TISSUE-Glandular pool- thyroid;				CC		
RA	Strausberg R.;				CC		
RL	Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.				CC		
DR	EMBL; BC062704; AAH62704.1; -; mRNA.				CC		
DR	HSSP; P01837; ICRU.				CC		
DR	Q6P5SB; 21-236.				CC		
DR	InterPro; IPR003599; Ig-1-like.				CC		
DR	InterPro; IPR007110; Ig-1-like.				CC		
DR	InterPro; IPR00597; Ig-Cl.				CC		
DR	InterPro; IPR003006; Ig-MIC.				CC		
DR	PFam; PF07654; C1-set; 1.				CC		
DR	SMART; SM00409; Ig-2.				CC		
DR	SMART; SM00407; IgC1.				CC		
DR	SMART; SM00406; IgV.				CC		
DR	PROSITE; P850835; Ig_LIKE; 2.				CC		
DR	PROSITE; PS00290; Ig_MHC; UNKNOWN_1.				CC		
KW	Hypothetical protein.				CC		
SEQUENCE	236 AA; 25773 MW; 953E37BEB4FF5F27 CRC64;				CC		
Query Match	86.3%; Score 48.1; DB 2; Length 236;				RESULT 15		
Best Local Similarity	85.3%; Pred. No. 9.4e-42; Indels 1; Gaps 1;				KV3K_HUMAN	STANDARD; PRT; 128 AA.	
Matches	9; Mismatches 6;				ID	KV3K_HUMAN	
Qy	1 EIVLTQSPGTLSLSPGERATLSCRASQVSSESSYLYQKPCQAPRLIYATSSRATGIP 60				AC	P06311;	
Db	21 EIVLTQSPGTLSLSPGERATLSCRASQVSSESSYLYQKPCQAPRLIYASSRATGIP 80				DT	01-JAN-1988 (Rel. 06, Created)	
Qy	61 DRFGSGSGSGTDFLTLSRLEPDFAVYVQOYGSPP-CSFGGGTKEIK 108				DT	01-JAN-1988 (Rel. 06, Last sequence update)	
Db	65 DRFGSGSGTDFLTLSRLEPDFAVYVQOYGSNS 99				DS	19 kappa chain V-III region IARC/B141 precursor.	
Qy	61 DRFGSGSGSGTDFLTLSRLEPDFAVYVQOYGSPP-CSFGGGTKEIK 108				OS	Homo sapiens (Human).	
Db	65 DRFGSGSGTDFLTLSRLEPDFAVYVQOYGSNS 99				OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.	
Qy	81 DRFGSGSGSGTDFLTLSRLEPDFAVYVQOYGSPP-CSFGGGTKEIK 129				OC		
Db	81 DRFGSGSGSGTDFLTLSRLEPDFAVYVQOYGSPP-CSFGGGTKEIK 129				OC		
RESULT 14					OX	NCBI_TAXID=9606;	
KV3C_HUMAN					RN	[1]	
ID	KV3C_HUMAN	STANDARD;	PRT;	100 AA.	RP	NUCLEOTIDE SEQUENCE.	
RX	MEDLINE=86041852; PubMed=2997711;				RX		

Klobbeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.; "Human immunoglobulin kappa light chain genes of subgroups II and III." Nucleic Acids Res. 13:6499-6513 (1985).

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Search time : 139.592 secs